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GenCore version 5.1.7
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OM protein - protein search, using sw model

April 20, 2006, 09:35:12 ; Search time 109.906 Seconds Run on:

(without alignments)
971.459 Million cell updates/sec

US-10-634-108-4

1303 1 MRPQGPAASPQRLRGLLLLLL......GDASTGWNSVSRIIIEELPK 243 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2443163 Total number of hits satisfying chosen parameters:

2443163 seqs, 439378781 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\* Geneseg 21:\* Database

geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2003as:\* geneseqp2003as:\* geneseqp2003bs:\* ...... Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20058:\*

# SUMMARIES

	Description	Aab36667 Human sec	Abg96340 Human ova	Abj05554 Breast ca	Abb80978 Human REM	Abr58546 Human can		Abg75758 Human REM		Adb80510 Ovarian c	Adn39855 Cancer/an	Adn38732 Cancer/an		Adu23513 Alternati	Adu06493 Novel bro	Aeb28819 Human CTH	Aab08856 Amino aci	Aam25746 Human pro	Abg96338 Human ova		Adz51345 Amino aci		Adl71601 Novel hum	Abp68631 Human pan	Abj37031 Human bre
SUMMAKIES	ID	AAB36667	ABG96340	ABJ05554	ABB80978	ABR58546	ABR48227	ABG75758	ABU56607	ADB80510	ADN3 9855	ADN38732	ADL70254	ADU23513	ADU06493	AEB28819	AAB08856	AAM25746	ABG96338	ABR47627	ADZ51345	AAY91529	ADL71601	ABP68631	ABJ37031
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	o Query Match Length DB	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	278	278	278	278	278	243	243	278	243
	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.8	99.8	99.8	99.6
	Score	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1303	1300	1300	1300	1298
	Result No.		2	m	4	'n	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Aay99462 Human PRO Aay99441 Human PRO	Aab66190 Protein o Aab66211 Protein o	_	Human	Abgysyll Human sec Abb84939 Human PRO	Aae20462 Human tum	Abb95545 Human ang	Abp68636 Human pan	Human ]	Abu58582 Human PRO	Abu88130 Novel hum	Abu84445 Human sec	Abr66319 Human sec	Abr65709 Human sec	Abu99649 Human sec	Abj37761 Human tum	Abu82888 Human PRO	Abu90009 Novel hum
AAY99462 AAY99441	AAB66190 AAB66211	AAU29206	AAB87586	ABG95911 ABB84939	AAE20462	ABB95545	ABP68636	ABG78938	ABU58582	ABU88130	ABU84445	ABR66319	ABR65709	ABU99649	ABJ37761	ABU82888	ABU90009
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243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243	243
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25 26	27	5 6	30	31 32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1 AAB36667

000/5/01

AAB36667 standard; protein; 243 AA

AAB36667;

14-MAR-2001 (first entry)

Human secretory protein TGC-628 SEQ ID NO:7.

Human; secretory protein; cancer; immune disease; infectious disease; lung function disorder; liver function disorder; antiinflammatory; gastrointestinal disorder; oychetic; haematopoietic; anticoagulant; immunomodulatory; hepatotropic; cell proliferation-stimulant; cell migratory agent; cell differentiation-inducer.

Homo sapiens

WO200071581-A1.

19-MAY-2000; 2000WO-JP003221. 30-NOV-2000

99JP-00140229. 20-MAY-1999;

(TAKE ) TAKEDA CHEM IND LTD

g Mogi S, Tanaka H, Ohkubo S, Itoh Y,

콗

WPI; 2001-032023/04. N-PSDB; AAC90707.

Novel secretory protein and its salt with e.g. anti-cancer, anti-inflammatory and hematopoietic, effects, applicable as drugs in remedies and preventives to treat diseases like cancer and immune diseases.

Claim 1; Page 89-90; 122pp. Japanese.

AAC90701 to AAC90715 encode the human secretory proteins given in AAB36661 to AAB36675. The proteins can have cytostatic, anti-inflammatory, haematopoietic, anti-coagulant, immunomodulatory and heparotropic activities, and can be used as cell migratory agents, cell proliferation-stimulants and cell differentiation-inducers. The proteins are useful in the treatment and prevention of diseases such as cancer, lung function disorder, gastrointestinal disorder and immune diseases. AAC90716 to AAC90755 represent PCR primers

for assessing whether

us-10-634-108-4.rag

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The present invention relates to a new method into assessing wheener a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a control non-ovarian cancer sample, where the expression level of a marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer.) The cancer is gratients having a familial history of ovarian cancer (e.g. brain and central nervous system disorders (e.g. bacterial and cancer). The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and disorders (e.g. bacterial or viral maningtis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. bacterial or viral meningtis or encephalitis), inflammations (e.g. bacterial or viral meningtis or encephalitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be connecting a composition for inhibiting ovarian cancer, assessing the vorarian cancer, monitoring the progression of ovarian cancer, assessing the ovarian cancer has metastaalzed or is likely to metastasize, electing a composition for inhibiting ovarian cancer, assessing the ovarian cancer or at risk of developing ovarian cancer. The present amino acid cancer or at risk of developing ovarian cancer markers described in the sequence represents one of the ovarian cancer markers described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GVPGRDGSPGANGIPGTPGIPGFRGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
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assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.
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                                                                                                                                                                present invention relates to a new method
                                                                                                         English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Breast cancer-associated protein 19.
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                                                                                                              Disclosure; Page 252; 481pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; brain herniation schilis; connective tissue disorder; hear disorder; ischamic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                                                                                                                                   1 MRPOGPAASPORLRGILILILILOLPAPSSASEIPKGKOKAQLRQREVVDLYNGMCLQGPA 60
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), Mills GB;
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     which are used in the exemplification of the present invention
                                                                                                              Length 243;
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1 A, Vieby PO,
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Ar PJ, Sen A, Vieu
Glatt K;
                                                                                                           100.0%; Score 1303; DB 4;
100.0%; Pred. No. 1e-120;
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                                                                                                                                                                Mismatches
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, Morrisey MP, Olandt
Lu K, Schmandt RE, Zh
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14-MAR-2001; 2001US-0276026P.
10-AUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-0323580P.
26-SEP-2001; 2001US-0324967P.
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                                                                                                                                                                   Conservative
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                                                                                                                                    Similarity
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                                                          Sequence 243 AA;
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                                                                                                                                 Local Simi.
hes 243;
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Meyers RE,
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240 240

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Gaps

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DB 5; Length 243; Indels

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                The invention comprises a method of detecting a breast cancer-associated transcript in a cell from a patient. The method of the invention involves contacting a biological sample from the patient with a nucleotide that hybridises to one of the 69 breast cancer-associated gene sequences shown in the specification. The method of the invention is useful in the diagnosis or prognosis of breast cancer, and for detecting genes that are up or down-regulated in breast cancer cells. Genes identified by the method of the invention can be used in diagnostic purposes and also as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESPEESWIPNYKQCSWSSLNYGIDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKIAECTFTKORSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                           targets for screening for therapeutic compounds that modulate breast cancer (e.g. hormones or antibodies). Identification of genes that are over or under expressed in breast cancer can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure and biosensor development. Amino acid sequences ABU05516 - ABU05604 represent the proteins encoded by the 69 breast cancersesociated genes of the invention
                                                                                                                                                                                                                                                     Detecting a breast cancer-associated transcript in a patient's cell, useful for diagnosing breast cancer, comprises contacting a biological sample with a polynucleotide that selectively hybridizes with breast cancer nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESPEESWTPNYKQCSWSSLAYGIDL
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100.0%; Pred. No. 1e-120;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                             Disclosure; Page 364; 414pp; English.
                                                                                                                                                                        (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                  2001US-0265928P.
2001US-00829472.
                                                                                                                         09-APR-2001; 2001US-0282698P.
                                                                                                                                                29-MAY-2001; 2001US-0294443P.
                                                                  24-JAN-2002; 2002WO-US002242
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Matches 243; Conservative
                                                                                                                                                                                                                    2002-583738/62.
                                                                                                                                                                                            Gish KC,
                                                                                                                                                                                                                                N-PSDB; ABT07711
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                      WO200259377-A2.
Unidentified.
                                                                                                     02-FEB-2001;
                                                                                                                09-APR-2001;
                                             01-AUG-2002
                                                                                                                                                                                             Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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The invention traiters to mammatian carbonatus at the invention traiters. On mammatian carbonatus and encourage polymucleotides. REWODELIN is used to disgance atterial restenosis, negative remodeling or fibrosis, bone disease such as osteogenesis comprised to 1, collagen disease such as Oi, dystrophic epidermolysis bullosea (DEB) and Bethlem myopathy in a mammal. The polymucleotides are bullosea (DEB) and Bethlem myopathy in a mammal, where the cellular complexity of steopontin is dependent on Chial. Congositions of osteopontin, alkaline phosphatase or bone morphogenic protein correspontin, biglycan, alkaline phosphatase or bone morphogenic protein comprising antisense REWODELIN sequences are useful for treating diseases mediated by abnormal expression of a REWODELIN molecule in a human such as impaired wound healing, fibrosis of an organ, ectopic ossification, or hypertrophic scar formation. REWODELIN is useful in the development of collular signaling, advential fibrosis, negative remodeling and arterial remodeling and useful in gene therapy. REWODELIN is useful for elucidating the function of REMODELIN molecules in a cell, to identify a compound that affects (FEMODELIN expression and/or TGF-bet signaling, as a potential correspentic drup candidate for arterial restenosis, anti-cancer therapy, to promote or inhibit wound healing, to inhibit scar tissue or keloid for mammal. It is also useful for producing carecombinant cell and transgenic non-human mammals which are useful tools correspentics for treatment, and for elucidating the cellular roles of therapeutics for treatment, and for elucidating the cellular roles of therapeutics for treatment, and for elucidating the cellular roles of therapeutics for treatment, and for elucidating the cellular roles of therapeutics for treatment sequence represents a human REMODELIN polypeptide controles for treatment represents a human REMODELIN polypeptide controles for treatment sequence represents a human REMODELIN polypeptide controles for treatment sequence or decrease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New mammalian REMODELIN polypeptide for diagnosing arterial restenosis, negative remodeling, fibrosis, collagen disease, and bone disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to mammalian REMODELIN polypeptides and encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRPQGPAASPQRLRGLLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
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                                                                                                                                                                                                                                                                                                                                                                    vasotropic; cytostatic; osteopathic; collagen;
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100.0%; Pred. No. 1e-120;
ive 0; Mismatches 0
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ABB80978 standard; protein; 243 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-OCT-2001; 2001WO-US050940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-OCT-2000; 2000US-00692081.
                                                                                                                                                                                                                                                                         Human REMODELIN polypeptide
                                                                                                                                                                                                                                                                                                                                                                    REMODELIN; vulnerary; vaso
gene therapy; bone; human
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Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                  21-OCT-2002
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                                                                                           ABB80978;
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RESULT 6
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regulated in specific cancers (e.g. about 1031 genes up-regulated in
actute lymphocytic leukemial, ACC72641 to ACC72660 represent cancer
related gene nucleotide sequences which encode the proteins given in
ABR58521 to ABR58709. Also described: (1) determining the presence or
comprising a nucleotide acid molecule described above, (3) a host cell
comprising the vector; (4) an isolated polypeptide, which is encoded by
the nucleic acid; (5) an antibody that specifically binds the polypeptide
(4); (6) specifically targeting a compound to a pathological cell in a
patient by administering to the patient the antibody above; and (7) a
drug screening assay. The nucleic acid is useful as diagnostic markers or
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                                          GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE
                    GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL
                                                                                                                                                                                          GSPEMNSTINIHRISSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New genes that are up-regulated or down-regulated in cancers, useful a
markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
therapeutic targets for screening drugs for treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, cancer; diagnosis; screening; modulator; leukaemia; ischaemia; heart disease; atherosclerosis; endometriosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related protein SEQ ID NO:203.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 736; 767pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               ABR58546 standard; protein; 243 AA
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13-NOV-2001, 2001US-035066F.
08-FEB-2002, 2002US-035145P.
08-FEB-2002, 2002US-035252FP.
12-APR-2002, 2002US-0372246P.
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N-PSDB; ACC72666.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-2002;
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ABR58546
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                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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therapeutic targets. In particular, the nucleic acid is useful for diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow, bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary, pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases, atherosclerosis and endometricais. The nucleic acid is also useful in drug screening, particularly for identifying agents for treating these
                                                                                                                                                                                                                                                                                                          61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL
                                                                                                                                                                                                                                                                                                                           GVPGRDGSPGANGIPGTPGTPGFRGEKGEKGEKTRESFEESWTPNYKQCSWSSLNYGIDL
                                                                                                                                                                                                                                                                                                                                                                           121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCORWYFTFNGAECSGPLPIEAIIYLDQ
                                                                                                                                                                                                                                                                1 MRPQGPAASPORLRGLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
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                                                                                                                                                                                                                                           1 MRPGGPAASPORLRGLLLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
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                                                                                                                                                                      100.0%; Score 1303; DB 6; Length 243; 100.0%; Pred. No. 1e-120; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; bladder cancer; cytostatic; gene therapy; vaccine
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2001US-0310099P.
2001US-0343705P.
2001US-0350666P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                          Best Local Similarity 100. Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPK 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 LPK 243
                                                                                                                                        Sequence 243 AA;
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08-NOV-2001; 2
13-NOV-2001; 2
12-APR-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2001;
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                                                                                      drug screen:
pathologies
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                                                                                                                                                                          Query Match
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polymucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059 concode the human bladder cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated proteins given in haR848146 to have cytostatic activities, and can be used in antisense gene therapy and can varied production. The method can be used in antisense gene therapy and cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGEKCIRESFEESWTPNYKQCSWSSLNYGIDL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adventitia induced bone expressed molecule; AIBE, TGF-beta; transforming growth factor beta; adventitia; vascular remodelling; restenosis; vascular injury; antisense therapy; TGF-beta signalling; TGF-beta receptor type II; arterial remodelling; bone formation; cartilage formation; osteogenesis imperfecta; Bethlem myopathy; dystrophic epidermolysis bulloses, negative remodelling; wound healing; arterial stenosis; fibrosis; calcification; transplant; heart valve transplant; osteopathic; antiarteriosclerotic; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG75758 standard; protein; 243 AA.
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and/or adventitia induced by transforming growth factor beta (TGF-beil).

which is important because proliferative events occurring in the adventitia contribute to vascular remodelling and restenois in response to vascular injury and TGF-beta has been shown to be a factor involved in this. Also disclosed is an antibody raised against REMODELIN and methods for treating a disease mediated by abnormal expression of a REMODELIN in a cell (e.g. antisense therapy), for identifying a compound that affects or reduces expression of that affects TGF-beta signalling and for increasing or reducing REMODELIN expression in a mammal, comprising administering a REMODELIN expression or increasing or reducing TGF-beta to the mammal, thereby increasing creating receptor type II and reducing expression of REMODELIN in the mammal. The methods arterial remodelling, formation of REMODELIN in the mammal. The methods arterial remodelling, formation of bone and cartilage and the diagnosis and treatment of disorders associated with aberrant expression of the present invention are useful for mediating and the diagnosis and treatment of disorders associated with aberrant expression of
                                                                                                                                                                                                 New isolated REMODELIN nucleic acid and polypeptide, useful for mediating arterial remodeling, formation of bone and cartilage, and the diagnosis and treatment of disorders associated with aberrant expression of
                                                                                                                                                                                                                                                                                                                                                          The invention discloses an isolated nucleic acid encoding a mammalian adventitia-inducible bone expressed molecule called REMODELIN (or REMODEL and/or adventitia induced bone expressed molecule, AIBE). REMODELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REMODELIN, such as osteogenesis imperfecta, dystrophic epidermolysis bullosea, Bethlem myopathy, negative remodelling, wound healing, arterial stenosis, vessel injury, fibrosis and calcification of a transplant,
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                                                                                        Lindner V, Friesel RE;
                                                                                                                                  2003-238238/23
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                    (LIND/) LINDNER V. (FRIE/) FRIESEL R
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N-PSDB; ADB80509.
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                                                                                                                              LPK 243
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05-SEP-2001;
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                                                                  Lung cancer-associated polypeptide; cytostatic; emphysema; atelectasis; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer, benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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                                         Lung cancer-associated polypeptide #200.
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                                                                                                                                                                                                                                                                                         10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339345P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                   (EOSB-) EOS BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                               2001US-0284770P.
            (first entry)
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Best Local Similarity
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                                                                                                                                                                                        WO200286443-A2.
                                                                                                                                                            Unidentified
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            02-APR-2003
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The invention relates to a method of detecting an ovarian cancerassociated transcript in a cell from a patient, by contacting a biological sample from the patient with a polymucleotide that selectively bypridizes to a sequence at least 80% identical to any of one of 80 mucleic acid sequences given in the specification. The method is useful in diagnosing ovarian cancer and in identifying and using agents and/or targets that inhibit ovarian cancer. The nucleic acid molecule, polypeptide and the antibody may also be used in detecting ovarian cancers, monitoring and early detection of relapse following treatment, enonitoring response to therapy, selecting patients for post-operative chemotherapy or radiation therapy, in selecting mode of therapy, determining tumour prognosis, early detecting mode of therapy, and and as vaccines. This sequence corresponds to one of the proteins used for the detection method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detecting an ovarian cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a polynucleotide that hybridizes to an ovarian cancer gene.
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                                                                                                                                                                                                   240
121 GKIAECTFTKWRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ
                                                                                                                                                               GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              post-operative chemotherapy; radiation therapy; tumour prognosis; pre-cancerous lesion detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; gene therapy; vaccine; ovarian cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovarian cancer-associated protein #37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADB80510 standard; protein; 243 AA.
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; 2001US-0317544P.
; 2001US-0350666P.
; 2002US-0372246P.
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100.0%; Score 1303; DB 7; Length 243;

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us-10-634-108-4.rag

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ADN38732;
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                                                                            61 GVPGRDGSPGANGIPGTPGIPGTPGIPGRDGPKGEKGECLRESPEESWTPNYKQCSWSSLNYGIDL 120
                                                                                                                121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
                                                                 GVPGRDGSPGANGI PGTPGI PGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
                                                                                                      GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCORWYFTFNGAECSGPLPIEAIIYLDO 180
                                                                                                                                           GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
                                              9
                                                                                                                                                                                                                                                                                                                      Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischeemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; terinal neovascularistation syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                             1 MRPGGPAASPORLRGLLLLLLLGLPAPSSASEIPKGKOKAQLRQREVVDLYNGMCLQGPA
                                                                                                                                                     GSPERNSTINIHRTSSVEGLCEGIGAGLVDVALWVGTCSDYPKGDASTGRNSVSRIIIEE
                           1 MRPQGPAASPQRLRGLILLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
          Gaps
                                                                                                                                                                                                                                                                                                         Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
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Pred. No. 1e-120;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                  ADN39855 standard; protein; 243 AA.
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Murray R, Watson SR,
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2002US-0347349P.
2002US-0355250P.
2002US-0356714P.
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2001US-0334393P.
2001US-0335394P.
2001US-0340376P.
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2002US-0397775P.
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          243; Conservative
Best Local Similarity
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10-JAN-2002;
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Mack DH,
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          Matches
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
of determining the presence or absence of a pathological cell in a
contention or by detecting a polypeptide of the invention. The
cinvention also relates to expression vectors and host cells comprising a
concleic acid of the invention; antibodies which specifically bind a
polypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and nucleic acids. The nucleic acids, polypeptides,
cantebodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistation syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
                                                                                                                                 Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWIPNYKQCSWSSLNYGIDL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 1303; DB 7; Length 243; Best Local Similarity 100.0%; Pred. No. 1e-120; Matches 243; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                              Claim 12; SEQ ID NO C225; 1385pp; English.
                                                                                                                                                                                 seful for diagnosing, prognosing or tr
nucleic acid in a biological sample.
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2003-468649/44
                                                N-PSDB; ADN39637
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whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a parthological call in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host calls comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; and enclate acids, polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and muchaic acids. The nucleic acids, polypeptides.

The antibodies and muchaic acids. The nucleic acids, polypeptides.

The antibodies and muchaic are useful for disgnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal also be useful in wound healing and in contrarection. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gish KC, Glynne R, Hevezi PA;
Wilson KE, Zlotnik A;
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Pred. No. 1e-120;
; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; SEQ ID NO 50; 1385pp; English.
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100.0%; Pref
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Murray R, Watson SR,
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10-JAN-2002, 2002US-0347349P.
08-FEB-2002, 2002US-0355250P.
13-FEB-2002, 2002US-0356714P.
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2002US-0368809P.
2002US-0370110P.
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2002US-0397775P.
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2001US-0340376P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADN38731.
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                                WO2003042661-A2.
Ното варіепв.
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29-MAR-2002;
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14-DEC-2001;
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                                                                  22-MAY-2003
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Mack DH,
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240
GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLF1EA11YLDQ 180
          GSPEWNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of the polypeptide encoded by cDNA clone AD12. This clone corresponds to an mRNA species that is differentially
                                     GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecule associated with stomach cancer, useful for preparing a composition for diagnosing or treating cancers such as
                                                                                                                                                                                                                        LBFL301; human; stomach cancer; diagnosis; cytostatic
                                                                                                                                                                                                      LBFL301 polypeptide, associated with stomach cancer.
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                                                                                                                                                                                                                                                                                                                                                                                        Zeng W,
                                                                                                                                              ADL70254 standard; protein; 243 AA.
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23-AUG-2002; 2002US-0405304P.
28-OCT-2002; 2002US-0421582P.
                                                                                                                                                                                                                                                                                                                       2002US-0402904P.
                                                                                                                                                                                                                                                                                                    14-AUG-2003; 2003WO-KR001653.
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                        Chung H,
                                                                                                                                                                                                                                                                                                                                                                     (GLDS ) LG LIFE SCI LTD.
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by the store corresponds to an mixed species that is differentially expressed in cancerous stomach tissue compared to healthy stomach tissue. Clones AD12 and CH4 ADL70255 are splice variants of a gene designated clones AD12 and CH4 ADL70255 are splice variants of a gene designated clones AD12 and CH4 ADL70255 are splice variants of a gene designated (13.75-fold) in gastric carcinoma samples compared to samples from healthy stomach tissue. Up-regulation of LBFL301 may therefore be diagnostic for scomach cancer. The predicted proteins aerocade by AD12 and CH4 ADL70256 are identical for the first 124 anino acids, while the last 13 amino acids of the CH4 protein are unique. Termination of the CH4 ADL70256 acids of the CH4 protein are unique. Termination of the CH4 ADL70256 acids of the proteins are weakly similar to the chymotrypain serine protease family signature and the NUDIX hydrolase family signature. The nucleic acids and proteins are weakly similar to the progression of stomach cancer in a sample. The proteins can be used as diagnostic agents which modulate protein level or activity, to identify binding partners, to raise antibodies, as therapeutic targets, and as diagnostic agents which modulate protein level or activity, to identify binding partners, to raise antibodies, as therapeutic targets, and as diagnostic agents which modulate protein level or activity, to identify binding partners, to raise antibodies, as therapeutic targets, and as diagnostic agents or markers of stomach cancer and other hyperplastic diseases. A claimed method for diagnosing disease state in a subject comprises determining the level of expression of the nucleic acid, where the disease state is stomach cancer, advanced gastric cancer or a malignant

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Matches 243; Conservative

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1 MRPQGPAASPQRLKGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 1 MRPQGPAASPORLRGLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to a novel monoclonal antibody that specifically binds to an oligomeric form of human STOP-1. Specifically, it refers to a STOP-1 polypeptide variant that cannot be secreted from a cell or form a disulfide bind with another STOP-1 protein. The present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to an oligomeric form of
or treating diseases
cancer, and in research
neoplasm occurring in soft tissue, bone, breast, cervix, colon, endometrium, oesophagus, kidney, larynx, liver, lung, omentum, ovary, pancreas, rectum, thyroid, myometrium, prostate, skin, small intestine, bladder, spleen or stomach.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STOP-1; tumour; angiogenesis; vasculogenesis; cytostatic; gene therapy.
                                                                                                                                1 MRPQGPAASPQRLKGLLLLLLLLLLQLPAPSSASEIPKGKQQKAQLRQREVVDLYNGMCLQGPA
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                                                                  100.0%; Score 1303; DB 8; 100.0%; Pred. No. 16-120; Winnstches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human STOP-1, useful for diagnosing, preventing involving angiogenesis and vasculogenesis, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative human STOP-1 protein SegID 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 3; 265pp; English.
                                                                                                                                                                                                                                                                                                                                                        ADU23513 standard; protein; 243 AA
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Hongo J, Lee C, Marsters S,
Varfolomeev E, Wolf B;
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                Conservative
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                                                                                     Best Local Similarity
Matches 243; Conserv
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                                                         Sequence 243 AA;
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pharmaceutical carrier, where the artagonist specifically binds STOP-1 and the binding can be inhibited by the monoclonal antibody, 6B12. As such, it provides methods for disquesing or monitoring a tumour in a patient, as well as methods for the prevention or inhibition of the tumour growth that overexpresses STOP-1. Furthermore, it provides a drug screening method for testing the activity of a candidate antagonist or agonist of STOP-1 such that it can be used to treat a disease or condition associated with excessive, inappropriate or uncontrolled angiogenesis and/or vasculogenesis in a mammalian subject, alternatively it can also induce angiogenesis in a mammalian subject, alternatively it can also induce angiogenesis in a patient that would benefit from increased angiogenesis. Accordingly, pharmaceutical compositions developed thereof exhibit cytostatic activities and can be used in gene therapy as angiogenesis stimulators or inhibitors. This polypeptide sequence is an alternative human STOP-1 protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 243;
composition comprising a STOP-1 antagonist and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1303; DB 8; Length
100.0%; Pred. No. 1e-120;
ive 0; Mismatches 0; Indels
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Rosenthal A,
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HEIDEN CASTANOS-VELEZ
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The invention relates to an isolated polypeptide (I) comprising a human cleaved collagen triple helix repeat containing 1 (CTHRCI) or an isolated mutant CTHRCI polypeptide (II) comprising substitution of a human CTHRCI collagen domain with a mouse collagen 1 alpha 1 collagen domain. (I) and the disease an effective administering to a human collagen domining the disease an effective administering to a human collagen with the disease an effective administering to a human collagen from from fibrosis, constrictive remodeling and restenosis.

(I) or (II) is useful for decreasing levels of bone morphogenetic protein (I) by a cell, increasing the level of a propeptide (chosen from procollagen and a propeptide of lyyl-oxidase) in a cell, increasing the level of procollagen formation by a cell, decreasing collagen formation by a cell, decreasing collagen formation by a cell, decreasing collagen formation by collagen formation, where the condition is condition mediated by collagen formation, where the condition is condition mediated by collagen formation, inflammation associated scarring, pulmonary fibrosis, and angioplasty-associated contacting the cell with (I) or (II). (I) is useful for involves contacting the cell with (I) or (II). (I) is useful for contacting a cell with a BMP1 inhibiting of collagen fibrils in a cell, which involves contacting and enlay inhibiting approperied lysyl-oxidase, and further where the lysyl-oxidase mediates cross-linking of collagen fibrils, thus inhibiting cross-linking of collagen fibrils, thus inhibiting a cell with a BMP1 inhibiting of collagen fibrils in the cell, becausing the level of bone morphogenetic protein of BMP1 in a mammal, increasing the level of bone morphogenetic protein of BMP4 in a mammal, increasing the level of BMP4 in a mammal, increasing the level of BMP4 in a mammal in need, and increasing cell increasing the level of BMP4 in a mammal in need, and increasing collagen fibrils, the septement of BMP4 in a mammal in neit expression of BMP4 in a mammal increasing the 
                                                                                                                                                                                                                                                                                                                                                       Novel isolated polypeptide comprising human cleaved collagen triple helix repeat containing 1 (CTHRC1) or isolated mutant CTHRC1 polypeptide, useful for treating or preventing disease mediated by collagen matrix production e.g. fibrosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 4; 115pp; English.
                                                                                                                                                                 (MAIN-) MAINE MEDICAL CENT RES INST.
                                                 2001US-00045992.
                                                                                                          18-SEP-2003; 2003US-0504107P
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Best Local Similarity 100.
Matches 243; Conservative
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                                                 19-OCT-2001;
18-SEP-2003;
                                                                                                                                                                                                                     Lindner V;
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                                                                                                                                                                                                            This invention relates to a novel isolated nucleic acid associated with bronchial cancer comprising 489 defined sequences given in the specification. The invention may be useful for the production of compounds with a cytostatic activity through the inhibition of expression or activity of tumour-associated proteins. The novel DNA sequences and the proteins/peptides encoded by them are used for detecting bronchial cancer or determining the risk of developing it and to screen for specific binding partners of the DNA or protein sequences, where the binding partners are potentially useful as agents for treating or specific binding partners. The DNA or protein sequences can also be used for prognosis, detection of metastases and for secondary treatment of tumours that have been stabilised or are no longer detectable). Detecting abnormal expression of the DNA sequences provides early diagnosis of bronchial cancers. The present sequence is that of a protein encoded by a novel bronchial cancer-associated human gene sequence of the
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                                                                             New nucleic acid, and derived proteins, useful for diagnosis of bronchial cancer and in screening for therapeutic and diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1303; DB 8; Length 243; 100.0%; Pred. No. 1e-120; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                 Claim 2; SEQ ID NO 717; 1381pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEB28819 standard; protein; 243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CTHRC1 protein SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wound healing; scarring.
2004-786403/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                         N-PSDB; ADU06006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPK 243
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Query Match

엄 ઠે 셤

8

181

셤 δ 셤 ઠે

δ

RESULT 15 **AEB28819**  120

9

Gape

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10-SEP-2004; 2004US-00939233.

US2005147602-A1. Homo sapiens

07-JUL-2005

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음 중

241 LPK 243 ||| 241 LPK 243

д

Search completed: April 20, 2006, 09:41:16 Job time : 112.906 secs

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i

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

April 20, 2006, 09:41:38; Search time 19.6941 Seconds (without alignments) 1187,191 Million cell updates/sec

US-10-634-108-4

1303 1 MRPQGPAASPQRLRGLLLLL......GDASTGWNSVSRIIIEELPK 243 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416

283416 seqs, 96216763 residues

Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
1: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	complement subcomp	collagen alpha 3(I		collagen alpha 1(I		alp		collagen alpha 3(I	alpha		hypothetical prote	hypothetical prote		collagen alpha 5(I	hypothetical prote	collagen alpha 1(V			collagen alpha 1(X	_	ಹ	3		hypothetical prote		•–		collagen alpha 1(I	T) 1 645 1 1000 1 100
SUMMARIES	ΙD	S29328	A45407	T20177	CGHU1S	T29031	A55267	S28791	сснизв	CGHU7L	S16366	T15268	T26185	T26184	S22917	T24482	A45748	I48103	A54849	A39762	T18594	T24769	CIHUOC	T26281	T27644	T29731	T31631	CGRT1S	S21626	
	DB	5	~	~	~	~	7	~	-	Н	7	7	N	7	-	7	7	7	7	7	~	~	Н	~	~	~	~	Н	7	•
	Length	246	1752	289	1464	327	754	888	1670	1466	1763	311	304	304	1691	300	920	1549	2944	178	325	428	245	358	298	310	458	671	1453	
•	% Query Match	10.1	6.6	9.8	9.8	•	9.7	9.6		9.5	•	9.5	9.4		9.4	9.4	9.4	9.4	9.4	9.3	9.3		9.5	٠	•	•	٠		9.5	
	Score	131.5	129	128	127.5	126	126	125	125	124	124	123.5	123	123	123	122.5	122.5	122.5	122	121	121	120.5	120	120	119.5	119.5	119.5	119.5	119.5	
	Result No.	1	7	Ю	4	ß	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	•

collagen col-34 -	hypothetical prote	collagen alpha 1(I	collagen alpha 1(I	collagen alpha 1(X	collagen alpha 2(X	hypothetical prote	collagen alpha 1(X	collagen alpha 1(I	collagen alpha 6(I	collagen alpha 1(I	collagen alpha 1(I	collagen alpha 1(I	collagen alpha 1(I	collagen alpha 1'(	pulmonary surfacta
JC1448	T29956	CGCH1S	CGB07S	CGHUIE	S37749	T24586	S46657	A27353	CGHU6B	CGMS4B	S40991	A61396	B40333	A40333	LNHUP1
7	~	-	н	-	N	~	7	N	Н	Н	N	~	ч	~	н
298	299	1042	1049	1806	177	290	330	488	1691	1669	1744	323	1486	1492	248
9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.1	9.0	0.6	9.0	9.0
119	119	119	119	119	118.5	118.5	118.5	118.5	118.5	118	118	117.5	117.5	117.5	117
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

```
C;Accession: S29328
R;Petry, F.; Reid, K.B.M.; Loos, M.
R:Petry, F.; Reid, K.B.M.; Loos, M.
Biochem. 209, 129-134, 1992
A;Title: Isolation, sequence analysis and characterization of cDNA clones coding for the ecerebellin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-246 <PET>
A;Residues: 1-246 <PET>
A;Cross-references: UNIPROT:Q02105; UNIPARC:UPI0000028DD0; EMBL:X66295; NID:g50228; PIDP
C;Superfamily: complement subcomponent Clq chain A; complement Clq carboxyl-terminal how
F;122-245/Domain: complement Clq carboxyl-terminal homology <ClQ>
complement subcomponent C1q chain C - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S29328; MUID:93011118; PMID:1396691
A;Accession: S29328
```

	2;	64
	Gaps	PAGVPG
246;	19;	GMCLQG
Length	Indele	REVVDLYN
DB 2;	32;	KAQLRQ
10.1%; Score 131.5; DB 2; Length 246; 38.5%; Pred No. 0.00025;	5; Mismatches	LPAPSSASEIPKGKQ
Query Match 10.1%; Rest Local Similarity 38.5%;	Matches 35; Conservative 5; Mismatches 32; Indels 19; Gaps	5 GPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG 64
Query N	Matche	ò

7 名	:
È	65 RDGSPGANGIPGTPGIPGRDGFKGEKGE 92
Ę	

A45407

Collagen alpha 3(IV) chain - sea urchin (Strongylocentrotus purpuratus)

Collagen strongylocentrotus purpuratus (purple urchin)

Cyspecies: Strongylocentrotus

Cyspecies: Strongylocentrotus

Cyspecies: A45407; A43903; A23940

Cyspecies: A45407; A43903; A23940

Cyspecies: Strongylocentrotus

Cyspecies: Strongylocentrotus

Cyspecies: Strongylocentrotus

Cyspecies: Strongylocentrotus

Ayreference number: A45407; MUID:93186842; PMID:8444899

Ayreference number: A45407; MUID:93186842; PMID:8444899

Ayreference number: A5407; MUID:93186842; PMID:8444899

Ayreference: Type: nucleic acid

Ayresidus: 1-1752 (SERP)

Ayresidus: Compared from NCBI backbone (NCBIP:126841)

Rywesel, G.M.; Etkin, M.; Benson, S.

Dev. Biol. 148, 261-272, 1991

Ayritle: Primary mesenchyme cells of the sea urchin embryo require an autonomously prodh

A;Reference number: A43903; MUID:92038439; PMID:1936564

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A; Molecule type: DNA
A; Residues: 1-45 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-34 <CH2>
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A;Residues: 1-34 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: S01143
A; Status: preliminary
A; Notecusion: A43903
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 'P', 633-L537,'G' <WES>
A; Cross-references: UNIPAR: UPI00007C802; GB:S64572; NID:g238616; PIDN:AAB20270.1; PID:
A; Notec sequence extracted from NCBI backbone (NCBIN:64572, NCBIP:64573)
A; Notec sequence extracted from NCBI backbone (NCBIN:64572, NCBIP:64573)
B; Venkatesan, M; De Pablo, F; Vogell, G; Simpson, R.T.
Proc. Natl. Acad. Sci. U.S.A. 83, 3351-3355, 1986
A; Title: Structure and developmentally regulated expression of a Strongylocentrotus purp A; Reference number: A23940; MUID:86205894; PMID:3458186
A; Accession: A23940
A; Molecule type: DNA
A; Residues: 742-812 <VEN>
A; Cross-references: UNIPARC: UPI00001773DF; EMBL:M13206
C; Reywords: colled coll) extracellular matrix; glycoprotein; trimer; triple helix
F; 29-161/Domain: anino-terminal nonhelical, NCI <NCI>F; 29-161/Domain: colled coll, extracellularical, NCI <NCI>F; 29-164/Domain: collagen IV carboxyl-terminal repeat <CTI>F; 1644-1748/Domain: collagen IV carboxyl-terminal repeat <CTI>F; 1644-1748/Domain: collagen IV carboxyl-terminal repeat <CTI>F; 129/Modified site: allysine (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C53B4.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T2017
R;Berka, M.
R;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rcession: T20177
A;Status: DNA
A;Residues: DNA
A;Residues: 1-289 <WILL>
A;Coss-references: UNIPROT:Q18799; UNIPARC:UPI0000080F8D; EMBL:Z68215; PIDN:CAA92453.1;
A;Experimental source: clone C53B4
C;Genetics:
A;Genetics:
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.9%; Score 129; DB 2; Length 17. Best Local Similarity 22.9%; Pred. No. 0.0038; Matches 47; Conservative 20; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
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Best Local Similarity
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Collagen alpha 1(I) chain precursor - human
NyAlternate names: procollagen alpha 1(I) chain
SySpecies applies (man)
CySpecies: Homo sapiens (man)
CySpecies: Homo sapiens (man)
CyBate: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 31-Dec-2004
CyAccession: 160114; S01143; A93335; 155254; A39943; 155237; A35233; S09400; B90567; S11
SySp493; 153466; A02852; 137247
R;D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
Gene 67, 105-115, 1988
A;Title: Complete nucleoride sequence of the region encompassing the first twenty-five e
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A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1.369, 12, 371-589 < DAL>
A; Cross-references: UNIPROT: P02452; UNIPROT: Q14992; UNIPROT: Q16053; UNIPROT: Q13896; UNIPROT: C153, 919-922, 1988
Biochem. J. 253, 919-922, 1988
A; Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human
A; Reference number: S01143; MUID: 89025644; PMID: 3178743
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A; Residues: 1-472 < TRO)
A; Cross-references: UNIPARC: UPI000016A6F9; EMBL: X07884; NID: g30015; PIDN: CAA30731.1; PIDN
A; Cross-references: UNIPARC: UPI000016A6F9; EMBL: X07884; NID: g30015; PIDN: CAA30731.1; PIDN
A; Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988
R; Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
Asture 310, 337-340, 1984
A; Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of
A; Reference number: A93335; MUID: 84270697; PMID: 6462220
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A;Residues 1-58, Q', 60-181 <CHU>
A;Cross-references: UNIPARC:UPIO000173B3C; EMBL:X00820; NID:G35657; PIDN:CAA25394.1; PIDI
B;Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.
A; Biol. Chem. 262, 15151-15157, 1187
A;Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh
A;Reference number: 155254; MUID:88033098; PMID:2822714
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A,Title: Regulatory elements in the first intron contribute to transcriptional control o A,Reference number: A39943; MUID:88097389; PMID:3480516
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Biol. Chem. 260, 2315-2320, 1985
A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter 8: A;Reference number: I55237; MUID:85130970; PMID:2857713
A;Accession: I55237
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A;Title: In vivo and in vitro noncovalent association of excised alphal(I) amino-termina rome, type VII.
A;Reference number: A35233; MUID:90202908; PMID:2318855
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A;Residues: 33-52 «MIX»
A;Cross-references: UNIPARC:UP10000173B3D
A;Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved
R;Weil, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.
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738 as Glu
Brunelli, P.C.; Motte
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A; Residues: 746-766, 78, 768-781
B; Choseler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
A; Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(1) chain of ty A; Reference number: A47426, MUID:93352646; PMID:8349697
A; Reference number: A47426
A; Residues: 1179-1276, H', 1278-1336, 1339-1387, R', 1389-1464 < CHE>
A; Residues: 1179-1276, H', 1278-1336, 1339-1387, R', 1389-1464 < CHE>
A; Cross-references: UNIPARC:UPIO00073A2A; GB:S64596; NID:9407889; PIDN:AAB27856.1; PID
A; Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A; Note: does not represent an experimentally determined sequence but three different mut
                                                                                                                                                                                                                                                A; Wolecule type: DNA
A; Residues: 472-594, R',596-607 < CH3>
A; Residues: 472-594, R',596-607 < CH3>
A; Cross-references: UNIPARC: UPIO00011F796, GB: K03178; GB: K03179; NID: g179612; NID: g17961
A; Cross-references: UNIPARC: UPIO00011F796, GB: K03178; DF: Compared translated the codon GGT for residue 595 as Pro
R; Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
Am. J. Hum. Genet. 46, 1034-1040, 1990
A; Title: Variable expression of osteogenesis imperfecta in a nuclear family is explaine.
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A; Residues: 710-720, FZ, 722-737, FZ, 739-745 < WAL>
A; Residues: 710-720, FZ, 10F10000173B4B
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
A; Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
R; Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Motte
Hum. Mol. Genet. 3, 2201-2206, 1994
A; Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the
A; Reference number: I54365; MUID:95187161; PMID:7881420
                          A,Note: sequence partially completed for missing nucleotides by A29439
R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
J. Biol. Chem. 260, 691-694, 1985
A;Title: Wultiexon deletion in an osteogenesis imperfecta variant with increased type A;Reference number: A22161; WUID:85104934; PMID:2981843
A, Cross-references: UNIPARC: UP10000173B4A, GB: K01228, NID: 9180391, PIDN: AAA51995.1;
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A;Experimental source: normal dermal fibroblast culture
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Pred. No. 0.0043;
2; Mismatches 22;
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A;Residues: 1179-1387, 'R', 1389-1464 <CH7>
A;Cross-references: UNIPARC:UPI0000173B4F
A;Experimental source: fetal cell 88-251
R;Cohn, D.H.; Apone, S.; Byre, D.R.; Starm
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A,Experimental source: fetal cell 86-237
A,Accession: D47426
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A,Experimental source: fetal cell 86-146
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A;Residues: 1179-1336,1339-1464 <CH6>
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A,Residues: 1179-1276,'H',1278-1464
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34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1179-1464 < CH4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A35336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: C47426
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                                                                                  A MAGEGRAGE HORSE 155-138 (MET.)

A MAGEGRAGE HORSE 155-138 (MET.)

A MAGEGRAGE TO THE ACTUAL OF THE
                          Fitle: A base substitution in the exon of a collagen gene causes alternative splicing; Reference number: $09400; MUID:89356643; PMID:2767050; Accession: $09400
8, 1705-1710, 1989
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----QGLP 504

Gaps

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A;Molecule type: mRNA
A;Residues: 1-888 «NAH»
A;Cross-references: UNIPROT:Q90796; UNIPARC:UPI00000FBAD3; EMBL:M88593; NID:g211619; PID
C;Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
F;665-887/Domain: fibrillar collagen carboxyl-terminal homology «FCC»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collagen alpha 3(IV) chain precursor, long splice form - human
N;Alternate names: Goodpasture antigen; procollagen alpha 3(IV) chain long splice form
N;Alternate names: Goodpasture antigen; procollagen alpha 3(IV) chain long splice form
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A54763; A43928; Ā44043; A45971; A39786
C;Accession: A54763; A43928; Ā44043; P45971; A39786
J. Biol. Chem. 269, 23013-23017, 1994
A;Title: Complete primary structure of the human alpha3(IV) collagen chain. Coexpression:
A;Reference number: A54763; MUID:9436494; PMID:8083201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Modecule type: mRNA
A; Residues: 1.1670 <MARX-
A; Cross-references: 1.1670 <MARX-
A; Cross-references: No. P. U. PROT: Q01955; UNIPARC: UPI0000173BE3; GB:X80031; NID:9577563; PID:97
A; Experimental source: kidney
B; Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey, C.D.
Clin. Invest. 89; 592-601, 1992
A; Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be the al
A; Reference number: A43928, MUID:92147878; PMID:1737849
A; Accession: A43928
A; Residues: 1331-1524, I', 1526-1670 <TUR>
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J. Biol. Chem. 267, 19780-19784, 1992
A;Title: Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpastur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Residues: 1386-1670 <QUI>
A,GTOSB-references: UNIPARC:UPI000016A42D, GB:M92993; NID:g177895; PIDN:AAA21610.1; PID:
A,Note: sequence_extracted from NCBI backbone (NCBIP:115597)
                               Rivah, H.D.; Barembaum, M.; Upholt, W.B.
J. Biol. Chem. 267, 22581-22586, 1992
A;Title: The chicken alphal(XI) collagen gene is widely expressed in embryonic tissues.
A;Reference number: S28791; MUD:93054557; PMID:1429607
A;Accession: S28791
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riguinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 269, 17358, 1994
A,Reference number: A44738, MUID: 94274734; PMID: 8006044
A,Contents: annotation; erratum; correction to intronic sequence in A44043
R;Bernal, D.; Quinones, S.; Saus, J.
J. Biol. Chem. 268, 12090-12094, 1993
A;Fitle: The human mRNA encoding the Goodpasture antigen is alternatively spliced.
A,Reference number: A45971; MUID: 93280184; PMID: 8505332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 POGPAA--SPORLRGLLLLLLLLQLPAPSSASEIPKGKOKAQLRQREVVDLYNGMCLQGPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 125; DB 2; Length 888;
Pred. No. 0.004;
4; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Reference number: A44043; MUID:93015826; PMID:1400291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            505 GAPGODGPPGHLGPPGLPGLKGDPGSKGEKG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       479 POGPAGKPGPEGLRGI------PGPVGE-
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9.6%;
Best Local Similarity 35.2%;
Matches 32; Conservative
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A; Residues: 1427-1444 <BER>
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A;Residues: 1386-1670 <QUI:
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    C; Accession: S28791
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                                                                                                                                                                                                   hypothetical protein F53G12.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 12-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T29031
R;Wu, X.; Graves, T.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F53G12.
A;Reference number: Z20555
A;Reference number: Z20555
A;Reference number: Z20555
A;Retus: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: L327 < WUX>
A;Residues: L327 < WUX>
A;Residues: L327 < WUX>
A;Experimental source: strain Bristol N2; clone F53G12
A;Genetics:
A;Antrons: 59/3; 138/1; 223/2
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Collagen alpha 5(IV) chain - dog (fragment)

Collagen alpha 5(IV) chain - dog (fragment)

Cispectes Canis lupus familiaris (dog)

Cispectes on: A5267

Cispectes on: A526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRPQGPAASPQRLRGLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
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C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PQGPAASPQRLRGLLLLLLLLLQLPAPSSASEIP----KGKQ--KAQLRQREVVDLYNGMC
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Pred. No. 0.0027;
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    GNPGADGQPGAKGANGAPGIAGAPGFPGARG 416
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Local Similarity 35.4%; Pred. No. 0.00
tes 34; Conservative 7; Mismatches
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Matches 32; Conserv
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Best Local S:
Matches 34
    386
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요
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A,Accession: Course, Course, Full: PMID:2780304
A,Rocession: S04887
A,Rocession: S04887
A,Rocesternes: MRNA
A,Residues: 149-163, 'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634
A;Residues: 149-163, 'G',164-240,'D',242-471,'D',473-487,'L',489,'S',491-613,'Y',615-634
A;Roces-references: UNIPARC:UPI000016A61C; EMBL:X15332; NID:929945; PIDN:CAA33387.1; PII
A;Rores: the authors' translation of residues 905-932 is inconsistent with the nucleotid R;88-yer, J.M.; Kang, A.H.
A;Rores: Towarder: 1977
A;Atitle: Covalent structure of collagen: amino acid sequence of cyanogen bromide peptid. A;Reference number: A90399; MUID:77134724; PMID:S57335
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A;Residues: 'V',169-225,229-232,'P',234-292,'D',294-398 <SEY1>
A;Cross-references: UNIPARC:UP10000173B81
A;Experimental source: 11ver
A;Note: sequence corrected by A94562; attachment of 2-O-alpha-D-glucosyl-O-beta-D-galaci
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A; Reference number: A94562

A; Reference number: A94562

A; Accession: A94562

A; Molecule type: protein

A; Residues: 'V', 169-225, 229-277, 'A', 279-292,'D', 294,'S', 296-398 <SEY2>

A; Crose-references: Univer: 11ver: A; Note: author submitted corrections to A990399

A; Note: author submitted corrections to A990399

B; Milewicz, D.M.; Witz, A.M.; Smith, A.C.; Manchester, D.K.; Waldstein, G.; Byers, P.H.

Am. J. Hum. Genet: 53, 62-70, 1993

A; Title: Parental somatic and germ-line mosaicism for a multiexon deletion with unusual
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A; Residues: 186-194 <MIL>
A; Cross-references: UNIPARC:UP1000000B14; GB:S62925; NID:G386425; PIDN:AAD13937.1; PID
A; Cross-references: UNIPARC:UP100000B14; GB:S62925; NID:G386425; PIDN:AAD13937.1; PID
B; Chiodo, A.A.; Sillence, D.O.; Cole, W.G.; Bateman, J.F.
Biochem. J. 311, 939-943; 1995
A; Title: Abnormal type 1II collagen produced by an exon-17-skipping mutation of the COL?
A; Reference number: S59511; MUID:96067614; PMID:7487954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 302-423 <CHI>
A;Cross-references: UNIPARC:UP10000173B83; GB:S79877; NID:g1195576; PIDN:AAB35615.1; PIE
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: the complete sequence is not shown
R; Benson-Chanda, V.; Su, M.W.; Weil, D.; Chu, M.L.; Ramirez, F.
Gene 78, 255-265, 1989
A; Title: Cloning and analysis of the 5' portion of the human type-III procollagen gene A; Reference number: PE0011; MUID: 89378752; PMID: 2777083
A; Accession: PE0011
                                                                                                                                                                                                                                             A, Accession: S04642
A, Molecule type: mRNA
Residues: 1-1196 <ALA>
A, Cross-references: UNIPARC:UPI0000173B80; EMBL:X14420; NID:g30057; PIDN:CAA32583.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
A,Residues: 1-170 <704>
A,Cross-references: UNIPARC:UPI000016A706; EMBL:X07240; NID:930060; PIDN:CAA30229.1;
A,Note: the authors translated the codon CAG for residue 154 as His
R,Janeczko, R.A.; Ramirez, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Wolecule type: DNA
A; Residues: 1-176 < BEEN>
B; Roman, P.D.; Ricca, G.A.; de Crombrugghe, B.
Nucleic Acids Res. 16, 7201, 1988
A; Title: Nucleic de sequence of a cDNA coding for the amino-terminal region of human A; Reference number: S01726; MUID: 88303360; PMID: 3405773
R;Ala-Kokko, L.; Kontusaari, S.; Baldwin, C.T.; Kuivaniemi, H.; Prockop, D.J.
Biochem. J. 260, 509-516, 1989
A;Title: Structure of cDNA clones coding for the entire prepro-alphal(III) chain of
erences.
A;Reference number: S04642; MUID:89350838; PMID:2764886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17, 6742, 1989
A;Title: Nucleotide and amino acid sequences of the entire human alpha-1 (III)
A;Reference number: S04887; MUID:89386015; PMID:2780304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: I51868; MUID:93304430; PMID:8317500
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Seyer, J.M. submitted to the Atlas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AjGene: Gubicutata AjGenica (GDB:128351; OMIM:120070)
AjGross-references: GDB:128351; OMIM:120070
AjGross-references: GDB:128351; OMIM:120070
AjGross-references: GDB:128351; OMIM:120070
AjGross-references: GDB:128371; 14184/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete
AjNote: the alpha 31(1V) and alpha 41(1V) chain genes are encoded on opposite strands with
CjComplex: This minor type IV collagen is thought to form a heterotrainer of two alpha 30
CjComplex: This minor type IV collagen is thought to form a heterotrainer of two alpha 30
CjPunction:
AjDescription: minor structural component of extracellular basement membrane in kidney GC;Superfamily: collagen alpha 1(IV) chain
CjSuperfamily: collagen alpha 1(IV) chain
CjSuperfamily: collagen alpha 30
CjSuperfamily: collagen 10
CjSuperfamily: debodic 30
CjSuperfamily: d
                                             A; Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence incorrectly ident whorison, K.E.; Mariyama, M.; Yang-Peng, T.L.; Reeders, S.T. Am. J. Hum. Genet. 49, 545-554, 1991
A; Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain of A; Reference number: A39786; MUD:91353570; PMID:1882840
A; Accession: A39786
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(III) chain precursor - human N;Alternate names: procollagen alpha 1(III) chain C;Species: Homo sapiens (man) C;Date: 2-4Apr-1984 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004 C;Accession: S05272; S04642; FE0011; S01726; S04887; A90399; A94562; I51868; S59511; A999 R;Prockop, D.J. submitted to the EMBL Data Library, February 1989
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A;Accession: S05372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1240,'V',1242-1466 <PRC>
A;Coss-references: UNIPROT: P02461; UNIPARC: UPIO00000CDE; EMBL:X14420; NID:930057; PIDN
                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1453-1593'A',1595-1670 <MOR>
A;Cross-references: UNIPARC:UPI000014C40B; GB:S55790; NID:g234418; PIDN:AAB19637.1; PID:C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (ed and subsequently O-glycosylated.
C;Comment: In Goodpasture's syndrome, an autoimmune response develops against an epitope C;Genetics:
A;Gene: GDB:COLAA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --QGAAGLKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.6%; Score 125; DB 1; Length 16' Best Local Similarity 36.2%; Pred. No. 0.0083; Matches 34; Conservative 6; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467 GPKGEP----GLLCTQCPYIPGPPGLPGLPGLHGVKGIPGR--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 RDGSPGANGIPGTPGIPGRD---GFKGEKGECLR 95
A; Cross-references: UNIPARC: UP10000173BE5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
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A; Experimental source: liver
A; Note: the authors translated the codon TTC for residue 1057 as Tyr; the codons given f
                                                                                                                                                                                                                                                                                                                                                                                           C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (( 3-hydroxylated. About 15% of the lysines are 5-hydroxylated and some are subsequently O
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Access-references: GDB:118729; OMIM:120180
A,Cross-references: GDB:118729; OMIM:120180
A,Cross-references: GDB:118729; OMIM:120180
A,Cross-references: GDB:118729; OMIM:120180
A,Cross-references: GJ31-2431
A,Introns: 27/1; 94/3; 111/3; 149/3; 176/3; 554/3; 587/3; 1175/3; 1275/1; 1337/3; 1418/3
A,Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan A,Note: the list of introns is incomplete; defects in this gene can result in Ehlers-Dan C, their length, is formed with desmosine cross-links made from lysine and allysine r C,Function: structural component of extracellular fibrous polymer that maintains inte C,Superfamily: collagen alpha 1(1) Chain; fibrillar collagen carboxyl-terminal homology; C,Keywords: coiled coil; Ehlers-Danlos syndrome; extracellular matrix; glycoprotein; hydisplanean; amino-terminal propeptide #status predicted <PRO>F;24-153/Domain: amino-terminal propeptide #status predicted <PRO>F;31-94/Domain: unino-terminal nonholical telopeptide ***
Fil68-1196/Region: maino-terminal nonholical telopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F.103-1037/Region: call attachment (R-G-D) motif
F.1107-1221/Region: carboxyl-terminal nonhelical telopeptide
F.1122-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F.1222-1466/Domain: carboxyl-terminal propeptide #status predicted <CPR>
F.1238-1466/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
F.24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F.153-154/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicter
F.154/Modified site: allysine (Lys) #status predicted
                                                                                                                        A;Residues: 1176-1240,'V',1242-1356,'P',1358-1466 <CHU>
A,Cross-references: UNIPARC:UP10000173889; GB:M10615; GB:M10793; GB:M10794; GB:M10795;
        procollagen genes are located on the long PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen alpha 2(IV) chain precursor - pig roundworm
(Species: Ascaris suum (pig roundworm)
(Species: Ascaris suum (pig roundworm)
(Spacies: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
(Shacession: S16366
R;Pettitt, J.; Kingston, I.B.
J. Biol. Chem. 266, 16149-16156, 1991
A;Title: The complete primary structure of a nematode alpha-2(IV) collagen and the A;Reference number: S16366; MUID:91340768; PMID:1714907
A;Accession: S16366
A;Accession: S16366
A;Residues: 1-1763 <JBI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 LDCPNP----EIPFGECCAVCPQPPTAPTRPPNGQGPQGPKGDPGPPGIPGRNGDPGIPG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQLPAPSSASEIPKGKQKAQLRQREVVDLY--NGMCLQGPAGVPGRDGSPGANGIPGTPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 IPGRDGFKGEKGECLRESF---EESWTPNYKQCSWSSLNYGIDLGKIA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.0%; Pred. No. 0.0088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Mismatches
        A;Title: Human alpha 1(III) and alpha 2(V)
A;Reference number: I59025; MUID:85216505;
A;Accession: I79359
                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1165-1196 <EMA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40; Conservative
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hypothetical protein W05B2.1 - Caenorhabditis elegans
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cispecies: Tables
Backerson of the EMBL Data Library, October 1996
A;Reference number: 22016
A;Reference number: 22016
A;Recession: T26185
A;Accession: T26185
A;Accession: T26185
A;Accession: T36185
A;Greule type: DNA
A;Residues: 1-304 <WILL>
A;Residues: 1-304 <WILL>
A;Residues: clone W05B2
Cispecimental source: clone W05B2
Cispecimental source: clone W05B2
Cispecimental source: clone W05B2
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NyAlternate names: procollagen alpha 5(IV) chain
NyAlternate names: procollagen alpha 5(IV) chain
S(Contains: collagen alpha 5(IV) chain precursor, leukocyte splice form
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S22917; A54365; Ā57079; A37122; I54317; A34850; S18850; I56971; I76598; A3=
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A;Residues: 1-304 <WIL>
A;Zross-references: UNIPROT:Q9XVG3; UNIPARC:UPI0000079930; EMBL:Z81138; PIDN:CAB03474.1,
A;Experimental source: clone W05B2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----APGPKGP 254
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26184
R;Gardner, A.
Submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PQGPAASPQRLRGLLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 POGPAASPORLRGLLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.4%; Score 123; DB 2; Length 304; Best Local Similarity 33.0%; Pred. No. 0.0018; Matches 30; Conservative 5; Mismatches 24; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 123; DB 2; Length 304;
Pred. No. 0.0018;
5; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 PÓGP------PGPAGSPGAPGGPGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------PGPAGSPGAPGGPGQAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Reference number: 220166
A,Accession: T26184
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 sgapgopgapgnpgapgopgosggagskgic 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 SGAPGQPGADGNPGAPGQPGQSGGAGEKGIC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 PGRDGSPGANGIPGTPGIPGRDGFKGEKGEC 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 PGRDGSPGANGIPGTPGIPGRDGFKGEKGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.4%;
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Best Local Similarity 33.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 POGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: W05B2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Gene: CESP: W05B2.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 3
A;Introns: 27/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 3
A; Introns: 27/3
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                                                            Cistoria: 229/3; 266/3; 305/3; 424/1; 489/1; 548/1; 656/3; 790/1; 991/1; 963/1; 658/2; 501lagen alpha 1(IV) chain (Cisuperfamily: collagen alpha 1(IV) chain (Cisuperfamily: collagen alpha 1(IV) chain (Cisuperfamily: collagen alpha 1(IV) chain #status cell binding; coiled coil; disulfid F;1-26/Domain: signal sequence #status predicted <8IG>
F;27-1763/Product: collagen alpha 2(IV) chain #status predicted <MAT>
F;27-1763/Product: collagen alpha 2(IV) chain #status predicted <MAT>
F;27-159/Domain: non-collagens MIH #status predicted <MH>
F;197-199/Region: cell attachment (R-G-D) motif (R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F59E12.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15268
R;Johnson, D.
A;Description: The BEMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid F59E12.
A;Reference number: 218318
A;Reference number: 218318
A;Reference number: 218318
A;Reference number: 218318
A;Reference number: 12568
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-311 <-JOH>
A;Residues: 1-311 <-JOH>
A;Residues: 1-311 <-JOH>
A;Residues: 1-311 <-JOH>
A;Chess-references: UNIPROT:001904; UNIPARC:UPI000007B0FF; EMBL:AF003386; NID:g2088833; C;Genetics:
Cross-references: UNIPROT: P27393; UNIPARC: UPI0000126D40; GB:M67507; NID: 9159648; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1499 PGLPGFPGIEGIPGPPGLPGPPGPPGPSXKDGFLLVKHSQTSEVPQCPPGMVKLWDG 1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1449 GPMGAP-GIRGEKGLPGLDGLPGPSG----PPGFAGAKGR----DGFPGQPGMPGEKGA 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1559 YSLLYIEGNEKSHNQDLGHAGSC----LSRFSTMPFLF-----CDVNNVCNYASRNDKSY 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---SEGGIEPYISRCAVCEA-PANVIAVHSQTI 1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGRDGS PGANGI PGT PGI PGRDGFKGEKGECLRESF --- - EESWTPNYKQCS ----W--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 WYFTFNGAECSGPLPIEALIYLDOGSPEMNSTINIHRTSSVEGLCEGIGAGLVDV---AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GPAASPQRLRGLLLLLLLQ-LPAPSSASEIPKGKQKAQLRQREVVDLYNGM-CLQGPAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNAC-----CQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 9.5%; Score 124; DB 2; Length 1763;
l Similarity 25.8%; Pred. No. 0.011;
67; Conservative 24; Mismatches 93; Indels 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 GMC-----LOGPAGVPGRDGSPGANGIPGTPGIPGRDGFKGEKGE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1610 WLST----TAPIPMMPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1652 QIPNCPN-----GWNSL 1663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 WVGTCSDYPKGDASTGWNSV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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A; Introns: 24/2
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Best Local Simi:
Matches 24;
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7

Gaps

62

--- APGPKGP 254

RESULT 12

3

32;

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A;Residues: 1284-1291, 'TFLGYLACLV' <GUO2>
A;Cross-references: UNIPARC:UP1000011DDFD, GB:S69169; NID:g545097; PIDN:AAC60613.1; PID: A;Cross-references: UNIPARC:UP1000011DDFD, GB:S69169; NID:g545097; PIDN:AAC60613.1; PID: A;Cross-references: UNIPARC:UP100011DDFD, GB:S69169; NID:g545097; DD:g546097; DD:g546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Mestadues: 1446-1477 ANE:
A; A; Ctross-references: UNIPARC: UDIO000173BE2
R; Nakazato, H.; Hattori, S.; Ushijima, T.; Matsuura, T.; Koitabashi, Y.; Takada, T.; Yos:
R; Makazato, H.; Hattori, S.; Ushijima, T.; Matsuura, T.; Koitabashi, Y.; Takada, T.; Yos:
R; Kaney Int. 46, 1307-1314, 1994
A; Title: Mutations in the COL4A5 gene in Alport syndrome: a possible mutation in primord)
A; Reference number: 156975; MUID:95156893; PMID:7853788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Accession: IS6975
A)Status: translated from GB/EMBL/DDBJ
A)Alcule type: DNA
A)Accession: 1595-1602
A)ACCESSION: 1595-1602
A)ACCESSION: 1596-1602
A)ACCESSION: IS4188; MUD:94010948; PMID:8406498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1664-1607, 'VHDAYKC: <LEM>
A;Cross-treferences: UNIPARC:UP1000011F85C; GB:S65767; NID:g425563; PIDN:AAD13967.1; PID:
A;Note: frameabilf mutation from a patient with Alport syndrome; five other mutations ar
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ayrobsertereness: User 1920-90; Unimic 1920-90 Ayrobsertereness: User 1920-1920 Ayrobsertereness: User 1920-1920 Ayrobsertereness: User 1920-1920 Ayrobsertereness: 27/3; 47/3; 77/3; 92/3; 1006/1; 1036/1; 1082/3; 1125/1; 1135/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 1185/1; 11
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Pred. No. 0.013;
7; Mismatches 38; Indels 10
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A,Gene: GDB:COL4A5, ATS
A,Cross-references: GDB:120596; OMIM:303630
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9.4%;
Best Local Similarity 36.5%;
Matches 35; Conservative
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7. Fign. Chem. 57. 1145:1441.136. Trygyvaeon. K.
7. Fign. Chem. 57. 1145:1441.136. Trygyvaeon. K.
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hypothetical protein T05A1.2 - Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Species: Caenorhabditis elegans
C'Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C'Date: 15-Oct-1999 #sequence 1989
A'RACCESSIO: T2482
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      1307 DQGPPGLQGNPGRPGLNGMKGDPGLPGVPGFPGMKG 1342
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T24482
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mus musculu caenorhabdi

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homo sapien

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MEDINE-2887296; PubMed=1297309; DOI=10.1101/gr.129003;
MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] [ISSPORM I]

MUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] [ISSPORM I]

A Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J.,

Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

A Baton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,

Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H.,

Vansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,

Mood W.I., Godowski P.J., Gray A.M.;

"The secreted protein discovery initiative (SPDI), a large-scale

The fefort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHR1 HUMAN

ID CTHR1 HUMAN

AC Q96GGB, QBIX63;

DT 10-MAY-2005 (Rel. 47, Last sequence update)

DT 10-MAY-2005 (Rel. 48, Last amotation update)

DT 13-SEP-2005 (Rel. 49, Last amotation update)

DT 13-SEP-2005 (Rel. 49, Last amotation update)

DT 10-MAY-2005 (Rel. 49, Last amotation update)
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PUBMEd=15618538; DOI=10.1161/01.RES.0000154262.07264.12;
Pyagay P., Heroult M., Wang Q., Lehnert W., Belden J., Liaw L., Friesel R.E., Lindner V.;
Friesel R.E., Lindner V.;
Friesel R.E., Lindner T.;

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Sanuki N., Fujiki K., Kanai A., Tanaka Y., Iwata T.;
"Novel polypeptide found in human cornea cDNA library.";
Submitted (UMN-2001) to the EMBL/GenBank/DDBJ databases.
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                             MOUSE
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MOUSE
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Q4RWT3 TETNG
Q4RXU1 TETNG
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BRARE
BRARE
MOUSE
TETNG
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Q8CD80 N
Q70575 N
Q0NW57 E
Q08RN9 N
Q01799 Q
Q6P4U1 E
Q6P4U1 E
Q6U175 E
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  568
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  \begin{matrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} 
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                                                                                                                                                                                          April 20, 2006, 09:35:42; Search time 151.835 Seconds (without alignments) 1129.140 Million cell updates/sec
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Q6ax10
Q8xx03
Q8xx03
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Q60108
Q6108
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Q4rmt1
Q86y22
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                             5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2166443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2166443 segs, 705528306 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  657475_HUMAN

057474_HUMAN

090052_HUMAN

061854_CAEBR

C10C_MOUSE

090026_CHICK

0482U5_TETNG

0802E

080726_STRPU

018799_CAEBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHR1_HUMAN
CTHR1_RAT
CTHR1_MOUSE
QSHZDZ_KENTR
Q4SMQ6_TETNG
Q6ASML0_BRARE
Q8KQ36_MOUSE
Q4RX03_TETNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q4RMT1_TETNG
Q86Y22_HUMAN
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8 HUMAN
5 HUMAN
HUMAN
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                             GenCore version
Copyright (c) 1993 - 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                            OM protein - protein search, using sw model
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06MEY7_P
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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Match Length DB
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1303 1225 1210 992 951 928 139

Result

133.5 133.5 133.5 133.5 133.5 133.5 130.5 130.5 120 120.5 127.5 12

sed

Minimum DB Maximum DB

Database

Perfect score:

Run on:

Sequence:

Scoring table:

protein

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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Nogeak S.A., McKernan K.J., Malek J.A., Gunzatene P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Petteman M., Madan A., Kodrigues S., Sanchez A., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein 1.
Collagen-like.
N-linked (GlCNAc. . ) (Potential).
MRPGGPAASPORLRGLLLLLLQLPAPSSASEIPKGKQKAQ
LRQREVVDL. -> MRPPGRSTTVKLREKTVSRKLEMNGPSA
FQGLLCGK (in isoform 2).
/FTId=VSP_013622.
K -> IYML (in isoform 2).
K -> IYML (in isoform 2).
G -> v (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen triple helix repeat-containing
                                                                                                                                                                                                                                                                                                           PROTEIN SEQUENCE OF 31-45 (ISOFORM 1).
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
-I-FUNCTION: May act as a negative regulator of collagen matrix deposition (By similarity).
-I-SUBCELLULAR LOCATION: Secreted; extracellular (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF0131); Collagen; 1.
Probom; PD00007; Collagen; 1.
Alternative splicing; Collagen; Direct protein sequencing;
Extracellular matrix; Glycoprotein; Signal; Structural protein.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tisola-096CG8-2; Sequence-VSP_013622, VSP_013623;
Note-No experimental confirmation available;
TISSUE SPECIFICITY: Isoform 1 is expressed in calcified atheroselerotic plaque and chondrocyte-like cells.
FTM: N-91ycosylated (By similarity).
SIMILARITY: Contains 1 collagen-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AllFFEBIC66867F9 CRC64;
                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=096CG8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AY358914; AAQ89273.1; -; mRNA.
EMBL; BC014245; AAH14245.1; -; mRNA.
Ensembl; ENSG0000164932; Homo aapiens.
HAC; HGNC; HGNC; 18831; CTHRC1.
InterPro; IPR008161; CIg helix.
InterPro; IPR008160; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY136825; AAN15749.1; -; mRNA.
EMBL; AF395488; AAO17919.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26224 MW;
                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
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186
50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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Gaps

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Indels

0; Mismatches

Matches 243; Conservative

Query Match Best Local Similarity

Score 1303; DB 1; Length 243; Pred. No. 2.2e-107;

100.0%;

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"Collagen triple helix repeat containing 1, a novel secreted protein
in injured and diseased arteries, inhibits collagen expression and
promotes cell migration."

Circ. Res. 96:261-268(2005).

Circ. Res. 96:261-268(2
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                                                                                                                                                                                                                                           180
                                                                                                                     120
                                                                                                                                                                                61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWIPNYKQCSWSSLNYGIDL 120
                                                                                                                                                                                                                                                                             121 GKIAECTFTKØRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
                                                                                                                                                                                                                                                                                                                                                                 181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
                                                                                                                                                                                                                                                                                                                                                                                                9
9
                                  1 MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
                                                                                                                     GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL
                                                                                                                                                                                                                                        121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvėgicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Glires; Rodentia, Sciurognathi;
Muroidea, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLECTIDE SEQUENCE [MRNA], POSSIBLE FUNCTION, N-GLYCOSYLATION, INDUCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
STRAIN-Sprague-Dawley, TISSUE-Carotid artery,
Pubmed-15618518; DOI=10.1161/01.RES.0000154262.07264.12;
Pyagay P., Heroult M., Wang Q., Lehnert W., Beiden J., Liaw L.,
Priesel R. B., Lindner V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2005 (Rel. 47, Created)
10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Collagen triple helix repeat-containing protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: N-glycosylated.
SIMILARITY: Contains 1 collagen-like domain.
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Ensembl; ENSRWCG0000004578; Rattus norvegicus.
RGD; 628801; Cthrc1.
INTERPO; IPRO08161; Clg helix.
InterPro; IPR008160; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01391; Collagen; 1.
ProDom; PD000007; Clg_helix; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 LPK 243
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                                                                                                                                                                                                                                                                                                                                                                                                   DLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLFIEAIIYL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLECTIDE SEQUENCE [LARGE SCALE MRNA].

NUCLECTIDE SEQUENCE [LARGE SCALE MRNA].

STRAIN=CSPAL/6J; TISSUE=Embryo;

NATAIN=CSPAL/6J; TISSUE=Embryo;

NATAIN=CSPAL/6J; TISSUE=Embryo;

NATAIN=CSPAL/6J; TUSNUE=LAL, Yamanta I., Kondo S.,

NATAIN=CSPAL/6J; THAND M., Kasukawa T., Adachi J., Bono H., Kondo S.,

NATAIN=CSPAL/6J; THAND M., Kasukawa T., Nogami A., Schonbach C., Gojobori T.,

NATAIN M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani D.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani D.E., Cousins S.,

An Garimond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

Kanai A., Kawaii H., Kawasawa Y., Kedzierski R.M., King B.L.,

Kanajaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Shanachandran S.,

Nagashima R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Narando M., Wannelseedt C., Sengel C., Wang L.,

Narando M., Wannelseedt C., Sengel C., Wang L.,

Narando M., Wannelseedt C., Sangle C., Wang L.,

Narando M., Shinada K.,

Nallana R., Taylor M.S., Taylor W., Shinada Y., Walls C.,

Willming L.G., Wynshaw-Boris A., Yangisawa M., Yang L.,

Narando M., Sakazume N., Sakazume N., Sakotume N., Sakotume N., Sakotume N., Sakotume N., Sakotume N.,
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                                                                                                                                                                                                                                                                     1 HIPQGRAASPQLLIGLFLVLLILLQLSAPSSASENPKVKQKALIRQREVVDLYNGMCLQG
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                                                                                                                                                                                                                                               1 MRPQGPAASPQRLRG--LLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQG
                                                                                                                                                                                                                                                                                                                         PAGVPGRDGSPGANGI PGTPG1 PGRDGFKGEKGECLRESFEESWTPNYKOCSWSSLNYG1
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Mammalia, Eutheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                            Gaps
                                                        helix repeat-containing
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                                                                                                                                                                                                          2;
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10-MAY-2005 (Rel. 47, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Collagen triple helix repeat-containing protein 1 precursor.
                                                                                                                                                                                                          Indels
                                   Potential.
Collagen triple helix repea protein 1.
Collagen-like.
N-linked (GlCNAC. . .) (Pot 4; 2296FD6DCDBA21F2 CRC64;
 Extracellular matrix; Glycoprotein; Signal;
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                                                                                                                                                                   Score 1225; DB 1;
Pred. No. 1.8e-100;
3; Mismatches 8;
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                                                                                                                                26424 MW;
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Best Local Similarity 94.7%;
Matches 232; Conservative
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                                      32
245
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188
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                   protein.
                                                                                                                                245 AA;
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188
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                     tructural pIGNAL
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Collagen;
                                                                                                               CARBOHYD
SEQUENCE
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J., Birney E., Hayashizaki Y.; The mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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Collagen triple helix repeat-containing protein I.
Collagen-like.
N-linked (GlCNAC. ..) (Potential).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                         extracellular (By similarity)
                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: May act as a negative regulator of collagen matrix
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Ensembl; ENSMUSG0000054196; Mus musculus.
MGI; MGI:1915838; CHNC1.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
ProDom; PR01991; Collagen.
ProDom; PR0000007; Clg helix; 1.
Collagen; Extracellular matrix; Glycoprotein; Signal;
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Last annotation update)
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Pred. No. 3.9e-99;
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93.5%; Pred. No. 3...
4; Mismatches
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10-MAY-2005 (TrEMBLrel. 30, Le
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IOCAS 8356 protein (Fragment).
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245
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                                                                                 TISSUE-Whole body:

X Staubberg S. D. Faingold E. A., Grouse L.H., Derge J. G.,

Altsubberg R.L., Feingold E. A., Grouse L.H., Derge J. G.,

Klausner R. D., Collins F. S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R. F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

Bitchenco L., Marusins K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

Roberzation and initial analysis of more than 15,000 full-length human
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Kitin S., Gerhard D.S.;
Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC089073; AAH89073.1; -; mRNA.
GO; GO:0005737; C:Cytcpplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clg helix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 AA; 28195 MW; F2E13334A1BA2CCA CRC64;
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 8 SCAF14545, whole genome shotgun sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.1%; Score 992; DB 2;
79.6%; Pred. No. 9.4e-80;
iive 22; Mismatches 21;
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  Kenopodinae; Xenopus; Silurana.
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ORFNames=GSTENG00015647001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 79.6
Matches 183; Conservative
                                                                     NUCLEOTIDE SEQUENCE.
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                   NCBI_TaxID=8364;
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1D 041
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Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Micaud S., Jaffe D., Fischer S., Lutfalla G., Dossat C., Segurens B.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanouba W., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
Benont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
R. Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
Rellis M., volff JN., Guigo R., Zody M.C., Mesirov J.,
Lindblad-Toh K., Birren B., Nubbaum C., Kahn D., Robinson-Rechavi M.,
Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Lander B.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 SLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SLNYGIDLGKVCDCTFTKLRSDSTLRVLFSGSLRLKCKNACCQRWYFTFNGAECTGPLPV 120
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Zgc:101075.
Zgc:101075,
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
Tetraodon nigroviridis (Green puffer).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Edilnopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes;
Tetradontoidea, Terraodontidae, Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope, Whitehead Institute Centre for Genome Research, Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

EMBL, CAARQ1014345, CAF98076.1; -, Genomic_DNA.

InterPro; IPR008161; Cla_helix.
InterPro; IPR008161; Cll_degn.
Probom; PD000007; Cll_degn.
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191 AA; 20525 MW; CAB7BF4F582A3AA6 CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.0%; Score 951; DB 2;
85.9%; Pred. No. 2.9e-76;
tive 17; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 164, Conservative
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|VSRVIIEELPK 191
                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
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    REPRESENTATION OF REPRESENTATI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 TKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNST 188
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4 KLTQLLICFWISLPPCVTQKAKERIPR-----QRDABFTDKYQA-CVQGVPGVQGRDGN 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57 PGINGIPGTPGIPGEDGLKGEKGECVSERFEEPWKPNFKQCAWNSLNYGIDLGKIAECTF
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Singapore local strain; TISSUS=Embryo;
Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC079494; AAH79494.1; -; mRNA.
ZFIN; ZDB-GENE-040808-22; zgc:101075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 AA; 25395 MW; 4F9C698080FE1F9B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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GO; GO:0006817; P:phosphate transport; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences."
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Q8K036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Muridae; Murinae; Mus.
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Name=Coll3al;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
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TISSUB-Manmary tumor. WAP-TGF alpha model. 7 months old;

WEDLINE-2238825; PubMedel2477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

Altegran R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

A Richards A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

G. Aller M., Schein J.B., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 PGAAGEOGPSGPKG-AKGEPGKGEMVD-YNGSINEALQEIRTLALMGPPGLPGQTGPPGP 450
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13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 11 SCAF14979, whole genome shotgun sequence.
ORFNames—GSTENCO0027621001;
Cretracdon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] -
NUCLEOTIDE SEQUENCE.
Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Mix FVE/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034164; AAH34164.1; -; mRNA.
MGI; MGI:1277201; Coll3a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             565 AA; 56726 MW; DBD3FF99D670195F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%; Score 139; DB 2; 34.8%; Pred. No. 0.0013; iive 12; Mismatches 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005911; C:intercellular junction; IDA.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
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ProDom; PD000007; Clg_helix; 1.
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Q4RX03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Conservative
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NUCLEOTIDE SEQUENCE.
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us-10-634-108-4.rup

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77 TPGIPGRDGFKGEKGE
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QSTAT4;
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    NUCLEOTIDE SEQUENCE.
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ses 33; Conserv
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SEQUENCE
                  Lawlor S.;
Submitted
                                                                                                                                                                              Collagen.
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Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
Anthouard V., Jubin C., Castelli V., Ratinka M., Vacherie B.,
Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
A cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
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Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
Mincker P., Landar E.S., Weissenbach J., Roest Crollius H.;
"Genome duplication in the teleost fish Tetraodon nigroviridis reveals
II. Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :| |:| : : : : |:| | 1107 ----SVAYMDASTGNLKKAVLLQGSNDV 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     958 PAGPAGSPGKDGPKGIRGDAGPPGRQGDAGLRG------PAGPSGEKGDAGEDGPVG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1067 PGLTGPAGELGRE-------FOVGDD--SLAPNTAAIQMTFLRLLSTEA- 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 DGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA-----ECTFTKWRSNSAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 RVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQGSPEMNSTINIHRTSSV 197
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KAQLRQREVVDL-----YNGMCLQGPAGVPGRDGSPGANGIPGIPGIPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Indels 102; Gaps
                                                                                                                                                                                                                              Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

C EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.

R EMBL/GABO101499; CAG07099.1; -; Genomic_DNA.

R InterPro; IPR008160; Collagen.

R InterPro; IPR008160; Collagen.

R Pfam; PF01410; ColLef; ib_collagen_C.

R Pfam; PF01410; ColLef; ib_collagen_C.

R Probon; PD000007; Clg_helix; 7.

R Probon; PD000180; Fib_collagen_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1208 AA; 115322 MW; 1551D2793FE52F6A CRC64;
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01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
020-lagen, type XIII, alpha 1 (Fragment).
Name=C01.311; ORFNames=RP11-26212.1-002;
Homo sapieng (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 10.4%; Score 135; DB 2; Local Similarity 23.2%; Pred. No. 0.0071; Ne 57; Conservative 24; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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OSTATS;
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                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Collagen.
SEQUENCE
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Matches
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34 PKGKQKAQLRQREVVDLYNG------G 76
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 PKGKQKAQLRQREVVDLYNG-------MCLQGPAGVPGRDGSPGANGIP----G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.2%; Score 133.5; DB 2; Length 652; Best Local Similarity 43.4%; Pred. No. 0.0047; Matches 33; Conservative 8; Mismatches 16; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 133.5; DB 2; Length 683; ilarity 43.4%; Pred. No. 0.0049; Conservative 8; Mismatches 16; Indels 19.
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL138925; CAL15452.1; -; Genomic_DNA.
EMBL; AC024601; CAL15452.1; JOINED; Genomic_DNA.
EMBL; AC025426; CAL15452.1; JOINED; Genomic_DNA.
EMBCH; PROGNOBLET TEA.
GO; GO:0006917; P:phosphate transport; IEA.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clg helix.
(MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                            652 AA; 63277 MW; BC950B456DBF34A6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Collagen, type XIII, alpha 1.
Name=COL1341; ORFNames=RP11-26212.1-004;
Homo sapiens (Human)
                       EMBL; AL138925; CAL15421.1; -; Genomic_DNA.
EMBL; AC024601; CAL15451.1; JOINED; Genomic_DNA.
EMBL; AC025426; CAL15451.1; JOINED; Genomic_DNA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008161; Clajhelix.
InterPro; IPR008161; Callagen.
PF01391; Collagen.
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                                                                                                                                                                                                                                                                                               ProDom; PD000007; Clg helix; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || || || || || 424 LPGPPGHDGEKGPRGK 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || || || || || 467 LPGPPGHDGEKGPRGK 482
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Pfam; PF01391; Collagen; 9. ProDom; PD000007; Clg_helix; 3.
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Q61BS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis briggsae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
NUCLEOTIDE SEQUENCE.
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wes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=CBG13239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C1QC MOUSE
Q02105;
                                               Collagen.
                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C10C_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          CORDITION
    8 % % S
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                                                                                                                                                                                                                                                                                                                                               셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| | : : |:|| ||| || 31 PKG-SKGEPGKGEMVD-YNGNINEALQEIRTLALMGPPGLPGGIGPPGAPGIPGQKGEIG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 PKGKQKAQLRQREVVDLYNG-----GMCLQGPAGVPGRDGSPGANGIP-----G 76
                                                                                                                                                                                   Nāme=COL13A1; Synonyms=COLXIIIA1;
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.2%; Score 133.5; DB 2; Length 717; 43.4%; Pred. No. 0.0052; Live 8; Mismatches 16; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (Jul. 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ293624; CAC00688.1; -; mRNA.
Ensembl; ENSGONO0197467; Homo sapiens.
HGNC; HGNC: 2190; COL13A1.
GO; GO:0005737; C:Cytoplasm; IEA.
GO; GO:000515; P:protein binding; IEA.
InterPro; IPR008161; Call adhesion; IEA.
InterPro; IPR008161; Callagen.
                                                                                                                                                                                                                                                                                                                                                                  Snellman A., Tu H., Vaeisaenen T., Kvist A.P., Huhtala P.,
Pihlajaniemi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; AL138925; CAL15450.1; -; Genomic_DNA.
EMBL; AC024601; CAL15450.1; JOINED; Genomic_DNA.
EMBL; AC024245; CAL15450.1; JOINED; Genomic_DNA.
HGNC; HGNC:2190; COL13A1.
GO; GO:0005737; C:Cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 AA; 69964 MW; A311E9C7D3E87577 CRC64;
                                                                                        01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2004 (TrEMBLrel. 26, Last annotation update)
Type XIII collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2005 (TrEMBLrel. 29, Created)
01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
Collagen, type XIII, alpha 1.
Name=COL1311, ORFNames=RP11-26212.1-001;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  717 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF01391; Collagen; 9. ProDom; PD000007; Clg_helix; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              489 LPGPPGHDGEKGPRGK 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 TPGIPGRDGFKGEKGE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 43.4%;
nes 33; Conservative
                                             Q9NQ52 HUMAN PRELIMINARY;
Q9NQ52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSTAT6 HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEOUENCE.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                          HUMAN
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Matches
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    RESULT 11
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431 PKG-SKGEPGKGEMVD-YNGNINEALQEIRTLALMGPPGLPGQIGPPGAPGIPGQKGEIG 488
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                                                                                                                                                                                                                         34 PKGKQKAQLRQREVVDLYNG------G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 POGPAASPORLRGLILLILLILLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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01-JUL-1993 (Rel. 26, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Complement Clq subcomponent, C chain precursor.
Name=clqg; Synonyms=Clqc;
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The C.briggaae Sequencing Consortium; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                  19;
                                                                   Query Match 10.2%; Score 133.5; DB 2; Length 717; Best Local Similarity 43.4%; Pred. No. 0.0052; Matches 33; Conservative 8; Mismatches 16; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary data.

RMED; CARCO100063; CASG/676.1; -; Genomic_DNA.

RGG; GO:0005737; CC3tcplasm; IEA.

RGG; GO:0004302; F:structural constituent of cuticle; IEA.

RGG; GO:0006817; P:phosphate transport; IEA.

RINEPPRO; IPR00486; Collagen.

R InterPro; IPR00486; Collagen.

R Pfam; PF01391; Collagen.

R Pfam; PF01484; Collagen.

R Pfam; PF01484; Collagen.

R Collagen; Hypothetical profesin.

SEQUENCE 289 AA; 28171 MW; 8C73D053AD817847 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 133; DB 2; Length 289; ilarity 33.7%; Pred. No. 0.002; Conservative 4; Mismatches 23; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 PGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239 SCAPCOPCANGNPGAPCOPCOSCERCIC-----PNY 272
717 AA; 69950 MW; FD12CA80CC93540F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein CBG13239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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NUCLECTIDE SEQUENCE [LARGE SCALE MENA].

NUCLECTIDE SEQUENCE [LARGE SCALE MENA].

NUCLECTIDE SEQUENCE—Colon, and Kidney;

NA Strauberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

An Expleton M., Soares M.B., Bonaldo M.F., Carahnof P.D., Heich F.,

Astapleton M., Soares M.B., Bonaldo M.F., Carahnof P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Tooshlyuki S., Carahnof P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Norley K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Nilalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffauc S., Sanchez A.,

Nhiting M., Madan A., Young A.C., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallus D.E.,

Bronnerch A., Schehn J.E., Jones B.J.M., Marra M.A.,

Bronnerch A., Schehn J.E., Jones H.D.,

Bronnerch A., Schehn J.E.,

Bronnerch A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                 STRAIN=ICR; TISSUB=Macrophage;
MEDLINE=93011118; PubMed=1396691;
Petry F., Reid K.B.M., Loos M.;
Isolation, sequence analysis and characterization of cDNA clones
coding for the C chain of mouse Clq. Sequence similarity of complement
subcomponent Clq, collagen type VIII and type X and precerebellin.";
Eur. J. Biochem. 209:129-134(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse CDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-1- FUNCTION: Clg associates with the proenzymes Clr and Cls to yield

-1, the first component of the serum complement system. The

collagen-like regions of Clg interact with the Ca(2+)-dependent

clr(2)Cls(2) proenzyme complex, and efficient activation of Cl

takes place on interaction of the globular heads of Clg with the

Pc regions of IgG or IgM antibody present in immune complexes.

-1- SUBUNIT: Cl is a calcium-dependent trimolecular complex of Clg, R

and S in the molar ration of 11:22. Clg subcomponent is composed

of nine subunits, six of which are disulfide-linked dimers of the

A and B chains, and three of which are disulfide-linked dimers of
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentía; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=BALB/c; TISSUE-Liver;
MEDLINE=96186528; PubMed=8666057; DOI=10.1007/8002510050077;
METLY F., McClive P.J., Botto M., Morley B.J., Morahan G., Loos M.;
"The mouse Clq genes are clustered on chromosome 4 and show conservation of gene organization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 Clq domain.
SIMILARITY: Contains 1 collagen-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP, Q60994; 1C28.
Ensembl; ENSMUSG0000036896; Mus musculus.
MGI; MGI:88225; Clqg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X66295; CAA46993.1; -; mRNA.
FMBL: X92960; CAA63535.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conservation of gene organization.";
Immunogenetics 43:370-376(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; BC043945; AAH43945.1; -; mRNA.; BC054443; AAH54443.1; -; mRNA.S29328; S29328;
                                                                                                                          NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the C chain.
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----AGCYGIPGMPGMPGAPG 47
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MEDLINE=21303548; PubMed=11274142; DOI=10.1074/jbc.M009912200;
Koch M., Foley J.E., Hahn R., Zhou P., Burgeson R.E., Gerecke D.R.,
Koch M.K., Foley J.E., Hahn R., Zhou P., Burgeson R.E., Gerecke D.R.,
"alpha 1(xx) collagen, a new member of the collagen subfamily, fibril-
associated collagens with interrupted triple helices.";
J. Biol. Chem. 276:23120-23126(2001).
EMBL; AF312825; AAK58847.1; -; mRNA.
HSSP; Q96KP7; IFNN.
Ensembl; ENSGALGO0000005797; Gallus gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GPAASPQRLRGILILILILILIQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                      Complement Cig subcomponent, C chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (B
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                                                                                                                                                                                                                                                                                                     Hydroxyproline (By similarity).
5-hydroxylysine (By similarity).
Hydroxyproline (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 246;
                                                                                                                 PERINTS; PRODOCO; COMPLEMNTCIQ.
PRODOM; PRODOCO7; Clg helix; 1.
PROSITE; PS50871; ClQ; 1.
Collagen; Complement pathway; Hydroxylation; Immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydroxyproline (By similarity). Interchain (with other C chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005737; C:cytoplasm; IEA.
GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
GO:0005198; F:structural molecule activity; IEA.
GO:0007155; P:cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2F79EA1274BCB8E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
11-DEC-2001 (TrEMBLrel. 26, Last annotation update)
COllagen type XX alpha | precursor.
Gallus gallus (Chicken).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 131.5; DB
Pred. No. 0.0022;
                                                                                                                                                                                                                                                                                      Clq.
Hydroxyproline (
Hydroxyproline (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1472 AA
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InterPro; IPR001073; C1q.
InterPro; IPR008161; C1g helix.
Pfam; PF00386; C1q; 1.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 RDGS---PGANGIPGTPGIPGRDGFKGEKGE
                                                                                                                                                                                                        Innate immunity; Plasma; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 AA; 25966 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35; Conservative
                                                                                                                                                                                                                                                                   1113
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DR GO; GO: 0006817; P:phosphate transport; IEA.

DR InterPro; IPR008161; Call helix.

DR InterPro; IPR008161; Call agen.

DR InterPro; IPR008161; FW III.

DR InterPro; IPR008129; Laminin G-TSP.N.

DR InterPro; IPR00321; WPR AI.

DR PEAM; PP00391; Call agen. 4.

DR PEAM; PP00391; Call agen. 4.

DR PEAM; PP00391; Call agen. 4.

DR PRANT; SM00000; C1g helix; 4.

DR SWART; SM00010; TSPN; 1.

DR SWART; SM0010; TSPN; 1.

DR SWART; SW00000; C1g helix; 4.

DR SWART; SW00000; C1g helix; 4.

DR SWART; SW0010; TSPN; 1.

DR SWART; TSPN; 1.

DR TRICTAGROSPERGE TSP
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Search completed: April 20, 2006, 09:49:21 Job time : 155.169 sec8

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; ORGANISM: Homo sapiens US-09-692-081-4
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TYPE: PRT
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                                                                                                                                                                                                                                                                        April 20, 2006, 09:49:46; Search time 27.6353 Seconds (without alignments) 726.976 Million cell updates/sec
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1 MRPQGPAASPQRLRGLLLLL......GDASTGWNSVSRIIIEELPK
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-09-489-47-205
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US-10-015-393A-432
US-10-015-393A-432
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US-10-014-804-958
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Maximum Match 100%
Listing first 45 summaries
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No.
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28 1046 80.3 197 2 US-10-076-622-516 Sequence 516, App 29 1046 80.3 232 2 US-09-834-759-517 Sequence 517, App 30 1046 80.3 232 2 US-076-622-517 Sequence 517, App 31 256 27.3 66 2 US-10-004-860-962 Sequence 962, App 32 256 27.3 66 2 US-10-004-860-962 Sequence 962, App 32 256 27.7 52 2 US-10-004-860-961 Sequence 961, App 34 296 22.7 52 2 US-10-004-860-961 Sequence 961, App 35 270 20.7 51 2 US-00-205-258-963 Sequence 961, App 36 22.7 51 2 US-10-004-860-961 Sequence 961, App 37 248 19.0 46 2 US-10-004-860-961 Sequence 961, App 40 20.5 16.9 52 2 US-09-205-258-969 Sequence 961, App 40 20.5 16.9 52 2 US-09-205-258-969 Sequence 960, App 40 20.5 16.9 52 2 US-09-844-740 Sequence 518, App 41 10.8 26 2 US-09-844-759-519 Sequence 519, App 54 111 10.8 26 2 US-09-844-759-519 Sequence 519, App 54 111.5 10.1 246 1 US-08-463-911-4
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### ALIGNMENTS

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Sequence 4, Application US/09692081

Sequence 4, Application US/09692081

Sequence 4, Application US/09692081

Sequence 4, Application US/09692081

Fatent No. 6630325

GENERAL INFORMATION:

APPLICANT: LINDNER, Volkhard

APPLICANT: ERIESEL, Robert F.

TILLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL

TILLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL

CURRENT APPLICATION NUMBER: US/09/692,081

CURRENT FILING DATE: 2000-10-19

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO 4
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100.0%; Pred. No. 5.3e-125;
ive 0; Mismatches 0;
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SEQ ID NO 352
LENGTH: 243
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; Sequence 514 Application US/09834759
; Patent No. 6660197
; GENERAL INFORMATION:
   APPLICANT: Joiang Viding Mitcham, Jennifer L.
   APPLICANT: Mitcham, Jennifer L.
   APPLICANT: Mitcham, Jennifer L.
   APPLICANT: Harlocker, Susan L.
   APPLICANT: Hepler, William T.
   APPLICANT: Hepler, William T.
   APPLICANT: Hepler, William T.
   APPLICANT: Hepler, William T.
   APPLICANT: Honderson, Robert A.
   TITLE OF INVENTION: COMPOSITION OF BREAST CANCER
   TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
   TITLE OF INVENTION: UNMBER: US/09/834,759
   CURRENT APPLICATION NUMBER: US/09/834,759
   CURRENT APPLICATION NUMBER: US/09/834,759
   CURRENT APPLICATION WIMBER: US/09/834,759
   CURRENT APPLICATION WIMBER: US/09/834,759
   CURRENT APPLICATION WIMBER: US/09/834,759
   SEQ ID NOS: 547
   SEQ ID NO 514
   LENGTH: 243
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TITLE OF INVENTION: 98 Human Secreted Proteins
             CURRENT APPLICATION NUMBER: US/09/489,847
CURRENT FILING DATE: 2000-01-24
EARLIER FILING DATE: 1999-07-29
EARLIER FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: PCT/US99/17130
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER APPLICATION NUMBER: 60/095,486
EARLIER FILING DATE: 1998-09-05
EARLIER FILING DATE: 1998-09-05
EARLIER PILING DATE: 1998-09-12
EARLIER PILING DATE: 1998-09-05
EARLIER PILING DATE: 1998-09-05
EARLIER FILING DATE: 1998-08-06
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Matches 242; Conservative
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; ORGANISM: Homo sapiens
US-09-834-759-514
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ORGANISM: Homo sapiens
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LPK 243
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APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurnet, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE PRIBARE PROBRE: P2830PLC23
CURRENT APPLICATION NUMBER: US/10/012,231A
CURRENT FILING DATE: 2002-06-10
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  Length 243
                                                          1; Indels
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Score 1294; DB 2;
Pred. No. 4.4e-124;
0; Mismatches 1;
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Fong, Sherman
Gao, Wel-Clang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
        99.38;
  Query Match
Best Local Similarity 99.64
Matches 242; Conservative
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Eaton, Dan 1.
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US-10-012-231A-352
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GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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APPLICANT: Hillan, Yames
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C23
CURRENT APPLICATION NUMBER: US/10/012,231A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 431
LENGTH: 243
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Pred. No. 4.4e-124;
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                                                                                                                                                       Sequence 431, Application US/10012231A Patent No. 6924355
GENERAL INPORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David APPLICANT: Desnoyers, Luc
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Fong, Sherman
Gao, Wei-Oiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
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Best Local Similarity 99.6%;
Matches 242; Conservative
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Eaton, Dan 1.
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ORGANISM: Homo Sapien
                                                                             241 LPK 243
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US-10-015-389A-352
; Sequence 352, Application US/10015389A
; Patent No. 6936436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

RESULT 6

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GVPGRDGSPGANGIPGTPGTPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
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APPLICANT: Pan, James
APPLICANT: Panni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2830P1C48
CURRENT APPLICATION NUMBER: US/10/015,389A
CURRENT APPLICATION TOWER: US/10/015,389A
CURRENT APPLICATION TOWER: US/10/015,389A
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 352
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APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC48
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                                    Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Gddard, Audrey
Godowski, Paul J.
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Fong, Sherman
Gao, Wei-Qiang
Gddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth J
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Desnoyers, L
Eaton, Dan l
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ORGANISM: Homo Sapien
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APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, Jämes
APPLICANT: Pan, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                                                               99.3%; Score 1294; DB 2; Length 243; 99.6%; Pred. No. 4.4e-124; ive 0; Mismatches 1; Indels
CURRENT APPLICATION NUMBER: US/10/015,389A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 431
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CURRENT APPLICATION NUMBER: US/10/006,768A
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 477
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 352
LENGTH: 243
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Matches 242; Conservative
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Matches 242; Conservative
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                                                                                                TYPE: PRT
ORGANISM: Homo Sapien
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US-10-015-389A-431
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pani, Names
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C10
CURRENT APPLICATION NUMBER: US/10/006,768A
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 477
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 431
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Pred. No. 4.4e-124;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 431, Application US/10006768A; Patent No. 6936697; GENERAL INFORMATION:
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Best Local Similarity 99.6%;
Matches 242; Conservative 0
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Eaton, Dan 1.
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APPLICANT: Gao, Wei-Cidang
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwark, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT
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                                 APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830PLC47
FILE REFERENCE: P2830PLC47
CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT APPLICATION NUMBER: US/10/015,671A
FILOR APPLICATION NUMBER: US/10/015,671A
PRIOR APPLICATION NUMBER: US/10/015,671A
PRIOR APPLICATION NUMBER: US/10/015,671A
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99.6%; Pred. No. 4.4e-124;
tive 0; Mismatches 1;
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Fong, Sherman
Gao, Wel-Qiang
Goddard, Audrey
Godowski, Paul J.
Gurmaldi, Christopher J.
Gurney, Austin L.
Godowski, Paul J. Grimaldi, Christopher J.
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APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
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Best Local Similarity 99.6
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
; ORGANISM: Homo Sapien
US-10-015-671A-431
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LENGTH: 243
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRPQGPAASPQRLRGLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
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CURRENT FILING DATE: 2001-12-11
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
LENGTH: 243
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99.3%; Score 1294; DB 2;
Best Local Similarity 99.6%; Pred. No. 4.4e-124;
Matches 242; Conservative 0; Mismatches 1;
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Sequence 431, Application US/10015671A

Petent No. 6946263

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Betsein, David

APPLICANT: Betsein, Dan I.

APPLICANT: Eaton, Dan I.

APPLICANT: Ferrara, Napoleone

APPLICANT: Foods, Sherman

APPLICANT: Foods, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gaodard, Audrey
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BACEr. Kevin P.
APPLICANT: Botstein, David
APPLICANT: Beton, Dan 1.
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddward, Audrey
APPLICANT: Goddward, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
                                                                                                                                                                 Sequence 352, Application US/10015671A Patent No. 6946263
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Hillan, Kenneth J.
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CORGANISM: Homo sapiens
US-10-015-671A-352
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             241 LPK 243
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-10-015-671A-352
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APPLICANT:
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GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2830PLC2
CURRENT APPLICATION NUMBER: US/10/011,833A
CURRENT FILING DATE: 2002-06-25
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
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Best Local Similarity 99.6
Matches 242; Conservative
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US-10-011-833A-431
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Perrara, Napoleone
APPLICANT: Fong, Met-Qiang
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grinaldi, Christopher J.
APPLICANT: Pan, James
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                                                                            Length 243;
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                                                                            99.3%; Score 1294; DB 2; 99.6%; Pred. No. 4.4e-124; ive 0; Mismatches 1;
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                                                                                                  Best Local Similarity 99.6
Matches 242; Conservative
       ; ORGANISM: Homo sapiens
US-10-015-393A-352
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ORGANISM: Homo Sapien
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US-10-015-393A-431
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GENERAL INFORMATION:

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APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Bestein, Dan I.
APPLICANT: Fong, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Andres
APPLICANT: Andres
APPLICANT: Acids Brooding the Same
FILE REFERENCE: P2830P1C2:
CURRENT APPLICATION NUMBER: US/10/011,833A
CURRENT PILING DATE: 2002-06-25
FILE REFERENCE: P282 ID NOS: 477
SEQ ID NO 4331
LENGTH: 243
FILE APPLICANT: Acids Brooding the Same
FILE REFERENCE: P2830P1C2: Acids Brooding the Same
FILE REFERENCE: P2830P1C2: Acids Brooding the Same
FILE REFERENCE: P2830F1C2: Acids Brooding 
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99.3%; Score 1294; DB 2; Length 243;
Best Local Similarity 99.6%; Pred. No. 4.4e-124;
Matches 242; Conservative 0; Mismatches 1; Indels C
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, ORGANISM: Homo Sapien
US-10-011-833A-431
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. . 13, Appl 12, Appl 30, Appl 31, Appl 31, Appl 8, Appl 964, Appl 33, Appl 375, Appl 273, Appl 376, Appl 376, Appl 376, Appl

Sequence Sequence Sequence

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Sequence Sequence Sequence

Sequence

4, Appli 41, Appl 1334, Ap 1434, Ap 911, App

Sequence Sequence

Sequence

Minimum DB Maximum DB

Database

Searched:

Sequence:

Run on:

Sequence

Sequence Sequence Sequence

Sequence

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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
TITLE OF INVENTION: MONBER: US,10/301,822
PRIOR PLING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR PLING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
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US-10-508-440-13
US-11-096-070-12
US-11-135-855-30
US-11-135-855-31
US-11-258-647-2
US-11-258-647-2
US-10-220-824-33
US-10-821-234-964
US-11-186-284-33
US-10-644-807-375
US-10-644-807-375
US-10-644-807-375
US-10-986-405-280
US-11-256-802-4
US-11-256-803-41
US-11-256-803-41
US-11-051-720-1334
US-11-051-720-1334
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SOFTWARE: FastSEQ for Windows Version 4.0
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1: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/2/pubpaa/US07 NEW_PUB.pep:*
4: /SIDS5/ptodata/2/pubpaa/US07 NEW_PUB.pep:*
5: /SIDS5/ptodata/2/pubpaa/US10 NEW_PUB.pep:*
7: /SIDS5/ptodata/2/pubpaa/US10 NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US11 NEW_PUB.pep:*
8: /SIDS5/ptodata/2/pubpaa/US11 NEW_PUB.pep:*
                               GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-195-883-366
US-10-195-883-366
US-11-102-240-122
US-11-103-195-122
US-11-226-869-514
US-11-226-869-514
US-11-226-869-515
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match Length DB
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US-10-063-703-122
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LENGTH: 243
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216 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 275
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                                                     GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE
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FILE REFERENCE: PSO31FIDID:
FULE REFERENCE: PSO31FIDID:
FULE REPERENCE: PSO31FIDID:
FURENT APPLICATION NUMBER: US/11/229,769
CURRENT FILING DATE: 2005-09-20
PRIOR APPLICATION NUMBER: 10/233,453
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 2000-01-24
PRIOR FILING DATE: 1999-07-30
PRIOR PRILING DATE: 1998-08-05
PRIOR PRILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 376
NUMBER OF SEQ ID NOS: 2.0
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Publication No. US20060079670A1
GENERAL INFORMATION:
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Best Local Similarity 99.6
Matches 242; Conservative
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US-11-229-769-205
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LPK 243
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LPK 278
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US-11-229-769-205
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US-11-080-991-14
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LENGTH: 243
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Sequence 14, Application US/11080991
Publication No. US20050266437A1
GENERAL INFORMATION:
APPLICANT: Veiby, Petter Ole
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: AND OVARIAN CANCER
TITLE OF INVENTION: AND OVARIAN CANCER
FILE REPERBENCE: MRI-039
CURRENT APPLICATION NUMBER: US/11/080,991
CURRENT PILING DATE: 2005-03-11
PRIOR PILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Eaton, Dan L.
APPLICANT: Gerritenen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrin L.
APPLICANT: Gurney, Auglin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
CHERENCE: PREFERENCE: P3230RIC1
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230RIC1
CURRENT APPLICATION NUMBER: US/10/063, 703
CURRENT PILING DATE: 2002-05-08
PRIOR APPLICATION FOR SECOND CONTRACTOR CON
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; ORGANISM: Homo sapiens
US-11-080-991-14
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ORGANISM: Homo Sapien
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61 GVPGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
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                                               Gaps
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99.6%; Pred. No. 1.6e-115;
tive 0; Mismatches 1; Indels
Length 243;
                                               1, Indels
Score 1294; DB 6;
Pred. No. 1.6e-115;
0; Mismatches 1;
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Query Match

Best Local Similarity 99.6%;
Matches 242; Conservative
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Watanabe, Colin K.
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Gurney, Austin L.
Pan, James
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Zhang, Zemin
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Goddard, Audrey
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US-10-195-883-366
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Best Local Similarity
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US-10-195-883-366
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                                                                                                                                                                61 GVPGRDGSPGANGIPGTPGIPGRDGPKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
                                                                                                         1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEI PKGKQKAQLRQREVVDLYNGMCLQGPA 60
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PAPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENERDE: PS440RIC312
CURRENT APPLICATION NUMBER: US/10/194,487
CURRENT FILING DATE: 2002-07-12
                                                                     1 MRPQCPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
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PRIOR PLING DATE: 2002-01-15

PRIOR PILING DATE: 2002-01-15

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-09-18

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-24

PRIOR PRILING DATE: 1997-10-24

PRIOR PILING DATE: 1997-10-24

PRIOR FILING DATE: 1997-10-21

PRIOR FILING DATE: 1997-10-28

PRIOR PRIOR PRICE DATE: 1997-10-28
                       Indels
  Best Local Similarity 99.6%; Pred. No. 1.6e-115; Matches 242; Conservative 0; Mismatches 1;
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Publication No. US20060074226A1
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
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Godowski, Paul J.
Gurney, Austin L.
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
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ORGANISM: Homo Sapien
US-10-194-487-366
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Best Local Similarity 99.6
Matches 242; Conservative
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; ORGANISM: Homo Sapien
US-10-195-889-366
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US-11-102-240-122
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Best Local Similarity
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith Victoria
APPLICANT: Smith Victoria
APPLICANT: Smith Victoria
APPLICANT: Weatanabe, Colin K.
APPLICANT: Weatanabe, Colin K.
APPLICANT: Shang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C324
CURRENT APPLICATION NUMBER: US/10/195,888
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER: OF SEQ ID NOS: 612
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99.3%; Score 1294; DB 6; Length 243;
Best Local Similarity 99.6%; Pred. No. 1.6e-115;
Matches 242; Conservative 0; Mismatches 1; Indels (
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10-195-889-366
15-405-889-366
1 Sequence 366, Application US/10195889
1 Publication No. US20060074227A1
1 GENERAL INPORMATION:
1 APPLICANT: Baker, Kevin P.
1 APPLICANT: Chen, Jian
1 APPLICANT: Gensioyers, Luc
1 APPLICANT: Goddard, Audrey
2 APPLICANT: Goddweki, Paul J.
2 APPLICANT: Gurney, Austin L.
3 APPLICANT: Smith, Victoria
3 APPLICANT: Smith, Victoria
                                                                                                                                                      Sequence 366, Application US/10195888
Publication No. US20060073545A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT CORGANISM: Homo Sapien US-10-195-888-366
241 LPK 243
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241 LPK 243
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LPK 243
                                                                                                                  RESULT 7
US-10-195-888-366
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LENGTH: 243
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sequence 122, Application US/11102240

sequence 122, Application US/11102240

publication No. US20050260647A1

GENERAL INFORMATION:

APPLICANT: Goddard, Audrey

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Gurney, Austin L.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: Goddard, Audrey

APPLICANT: BOOHAGEAL TUMOR

TITLE OF INVENTION: ANTIBOTIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS.

TITLE OF INVENTION: UNMBER: US/11/102,240

CURRENT APPLICATION NUMBER: 10/063662

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-102-06

PRIOR PILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 2000-08-24

PRIOR FILING DATE: 199-12-09

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 122

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181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C329
CURRENT APPLICATION NUMBER: US/10/195,889
CURRENT FILING DATE: 2002-07-15
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 366
SEQ ID NO 366
SEQ ID NO 366
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GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCORWYFTFNGAECSGPLPIEAIIYLDO 180
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181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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Publication No. US20060069054A1
GENERAL INFORMATION,
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Persing, David H.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REPRENCE: 210121.470C114
CURRENT APPLICATION NUMBER: US/11/226,869
                                                                                                                                                                                                                                   Sequence 514, Application US/11226869
Publication No. US20060069054A1
GENERAL INFORMATION:
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER FILE REPRENCE: 21012.1470C14
CURRENT APPLICAND NUMBER: US/11/226,869
CURRENT FILING DATE: 2005-09-13
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Pred. No. 1.6e-115;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 515
LENGTH: 278
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SOFTWARE: PastSEQ for Windows Version 4.0
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Best Local Similarity 99.6
Matches 242; Conservative
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ORGANISM: Homo sapiens
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US-11-226-869-515
                                                     LPK 243
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241 LPK 243
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                                                                                                                                                                                      RESULT 11
US-11-226-869-514
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US-11-226-869-515
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APPLICANT: GOGGGERIA POLITY
APPLICANT: GOGGGERIA POLITY
APPLICANT: GUINGA, AUGUST
APPLICANT: GUINGA, AUGUST
CULTGA, AUGUST
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TILLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230C16601
CURRENT FILING DATE: 2005-04-11
PRIOR APPLICATION NUMBER: 10/063743
PRIOR PLILOR DATE: 2002-05-09
PRIOR PLILOR DATE: 2003-06-09
PRIOR PLILOR DATE: 1998-04-22
PRIOR PLLING DATE: 1998-04-22
PRIOR PLLING DATE: 2000-08-24
PRIOR PLLING DATE: 2000-08-24
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Indels
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Mismatches
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Best Local Similarity 99.6%;
Matches 242; Conservative C
242; Conservative
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ORGANISM: Homo Sapien
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Publication No. US20060069054A1
| GENERAL INFORMATION:
| APPLICANT: HORDANTION:
| APPLICANT: Sleath, Paul R. |
| APPLICANT: Beath, Paul R. |
| TILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER |
| TILE REFERENCE: 210121.470C14 |
| CURRENT PAPLICATION NUMBER: US/11/226,869 |
| CURRENT FILING DAME: 2005-09-13 |
| NUMBER OF SEQ ID NOS: 627 |
| SEQ ID NO 5:6 |
| SEQ ID NO 5:6 |
| LENGTH: 197
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   Length 278;
                               1; Indels
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99.3%; Score 1294; DB 7;
99.6%; Pred. No. 1.9e-115;
iive 0; Mismatches 1;
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Pred. No. 4.7e-92;
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Best Local Similarity 99.5
Matches 196; Conservative
                             Matches 242; Conservative
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CORGANISM: Homo sapiens
US-11-226-869-516
 Query Match
Best Local Similarity
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US-11-226-869-516
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Sequence 517, Application US/11226869; Publication No. US20060069054A1

RESULT 14 US-11-226-869-517

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61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
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CANCER
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; Publication No. US20060069054A1
; GENERAL INFORMATION:
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Sleath, Paul R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR;
; TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF BREAST CAN;
; FILE REFERENCE: 2.10121.470C14
; CURRENT APPLICATION NUMBER: US/11/226,869
; CURRENT APPLICATION NUMBER: US/11/226,869
; NUMBER OF SEQ ID NOS: 627
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 518
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CAN
FILE REFERENCE: 210121.470C14
CURRENT APPLICATION NUMBER: US/11/226,869
CURRENT FILING DATE: 2005-09-13
NUMBER OF SEQ ID NOS: 627
SOUTHWARE: FastSEQ for Windows Version 4.0
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Matches 196; Conservative
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; ORGANISM: Homo sapiens
US-11-226-869-517
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Matches 46; Conserv
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243 4 US-10-063-547-122 Sequence 122, App 243 4 US-10-063-551-122 Sequence 122, App 243 4 US-10-174-590-366 Sequence 366, App 243 4 US-10-176-758-366 Sequence 366, App 245 Sequence 3	4 US-10-13-13-13-13-13-13-13-13-13-13-13-13-13-	4 US-10-176-483-366 Sequence 366, 4 US-10-176-749-366 Sequence 366, 4 US-10-176-914-366 Sequence 366,	4 US-10-10-915-356 Sequence 122, 4 US-10-063-513-122 Sequence 122, 4 US-10-063-515-122 Sequence 122, 4 US-10-063-515-122 Sequence 122, 5 US-10-063-515-122 Sequence 122, 5 US-10-063-515-132	4 US-10-103-706-166 Sequence 121, 4 US-10-173-706-366 Sequence 366, 4 US-10-175-752-366 Sequence 366,		ALIGNMENTS		on US/09829472A 0146862A1	t chnology, Inc. ethods of Diagnosis of Breast Cancer, Compositions and Methods of Screening for Modulators of Breast Cancer 1-0012000S UMBER: US/09/829,472A 2001-04-09	00-03-15 (00/6) 20 r. 2.1		8u	CN4, ESTB, E	100.0%; Score 1303; DB 3; Length 243; 100.0%; Pred. No. 1.6e-115; ative 0; Mismatches 0; Indels 0; Gaps 0;	MRPQGPAASPORLRGLLLLLLLLQLPAPSSASRIPKGKQKAQLRQREVVDLYNGMCLQGPA 60		GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLÆBSFERSWTPNYKQCSWSSLNYGIDL 120			GSPEMISTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIBE 240	IHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240		
28 1294 99.3 29 1294 99.3 30 1294 99.3 31 1294 99.3	1294 99	1294 99 1294 99 1294 99	1294 1294 1294 1294 99	1294 99			RESULT 1	Sequence 19, Application US/09829472A; Sequence 19, Application No. US20040146862A1; GENERAL INPORMATION:	APPLICANT: G18h, Kurt APPLICANT: G18h, Kurt APPLICANT: EOS Blotechnology, Inc. TITLE OF INVENTION: Methods of Diagnosis o TITLE OF INVENTION: Methods of Screening FILE REFERENCE: 018501-001200US CURRENT APPLICATION NUMBER: US/09/829,472A CURRENT APPLICATION NUMBER: US/09/829,472A DPIOD ADDITORION NUMBER: US/09/829,472A			ORGANISM: Homo sapie FEATURE:	; OTHER INFORMATION: BC US-09-829-472A-19	Query Match Best Local Similarity 100 Matches 243; Conservative	Oy 1 MRPQGPAASPC	Db 1 MRPGGPAASP	61	DD 61 GVEGKUGSFU	Db 121 GKIABCTFTRA	Qy 181 GSPEWNSTIN1	181	241 LPK 	Db 241 LPK 243
GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.	OM protein - protein search, using sw model	Run on: April 20, 2006, 09:50:45 ; Search time 92.1176 Seconds (without alignments) 1102.205 Million cell updates/sec	Title: US-10-634-108-4 Perfect score: 1303 Sequence: 1 MRPGSPAASPQRLRGLLLLLGDASTGWNSVSRIIIEELPK 243	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	hed: 1867569 seqs, 417829326 residues	er of hits s	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database: Published Applications AA_Main:* 1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:* 2: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:* 3: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:* 4: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:* 5: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:* 6: /cgn2_6/ptodata/1/pubpaa/USIO8_PUBCOMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	1303 100.0 243 3 US-09-829-472A-19 Sequence 1303 100.0 243 4 US-10-045-992-4 Semience	243 4 US-10-097-340-135 Sequence 243 4 US-10-295-027-50 Sequence 243 4 US-10-295-027-1173 Sequence	1303 100.0 243 4 US-10-173-999-74 Sequence 1303 100.0 243 4 US-10-058-270A-38 Sequence 1303 100.0 243 4 US-10-6734-10R-6 Sequence	1303 100.0 243 4 US-10-188-812-175 Sequence 1303 100.0 243 5 US-10-939-233-4 Sequence	1303 100.0 243 6 US-11-050-926-135 Sequence 1303 100.0 278 4 US-10-097-340-131 Sequence	1303 100.0 278 4 US-10-177-293-496 Sequence 1303 100.0 278 4 US-10-301-822-77 Sequence 1303 100.0 278 4 US-10-296-115-1261 Sequence	1303 100.0 278 5 US-10-961-139-2 Sequence 1303 100.0 278 6 US-11-050-226-131 Sequence	1300 99.8 243 4 US-10-351-334-205 Sequence 1300 99.8 278 4 US-10-060-036-4551 Sequence 1308 99.6 178-10-176-487-14 Seminance	1294 99.3 243 3 US-09-834-759-514 Sequence 1294 99.3 243 3 US-09-938-418-7 Sequence	1294 99.3 243 3 US-09-946-374-352 Sequence 1294 99.3 243 3 US-09-946-374-431 Sequence	1294 99.3 243 4 US-10-006-867-122 1294 99.3 243 4 US-10-052-886-366 1294 99.3 243 4 US-10-007-805-514

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JS-10-063-547-122	JS-10-063-551-122	JS-10-174-590-366	JS-10-176-758-366	US-10-175-737-366	US-10-063-616-122	18-10-174-581-366	US-10-176-483-366	US-10-176-749-366	US-10-176-914-366	US-10-176-915-366	US-10-063-569-122	8-10-063-513-122	US-10-063-515-122	US-10-063-512-122	US-10-173-706-366	JS-10-175-738-366	JS-10-175-752-366
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## ALIGNMENTS

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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

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                Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-188-812-175

US-10-188-812-175

US-10-188-812-175

US-11-050-926-135

US-11-050-926-135

US-10-177-293-496

US-10-177-293-496

US-10-296-115-1261

US-10-296-115-1261

US-10-296-113-1261

US-10-961-139-2

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                                                                                                                                                                                                                                                                                         1867569 seqs, 417829326 residues
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Publication No. US20040146862A1
GENERAL INFORMATION:
APPLICANT: Mack, David
APPLICANT: BCS Blackechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Breast Cancer, TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer; FILE REPRENCE: 018501-001200US
CURRENT APPLICATION NUMBER: US/09/829,472A
CURRENT APPLICATION NUMBER: US/09/829,472A
CURRENT APPLICATION NUMBER: US 09/525,361
PRIOR APPLICATION NUMBER: US 09/525,361
PRIOR PLING DATE: 2000-03-15
PRIOR FILING DATE: 2000-03-15
SOFTWARE.Patent IN Ver. 2.1
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100.0%; Pred. No. 1.6e-115;
tive 0; Mismatches 0;
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US-10-063-551-122
US-10-174-590-366
US-10-176-758-366
US-10-175-737-366
US-10-176-783-366
US-10-176-783-366
US-10-176-783-366
US-10-176-914-366
US-10-176-914-366
US-10-176-914-366
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US-10-175-788-366
US-10-175-782-366
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Best Local Similarity 100.
Matches 243; Conservative
   TYPE: PRT
ORGANISM: Homo sapiens
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61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
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GENERAL INCRAMINE

APPLICANT: Aziz, Natasha

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

APPLICANT: Havezi, Peter A.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Matson, Susan R.

APPLICANT: Matson, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: Matson, Susan R.

APPLICANT: Matson, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: Be blotechnology, Inc.

APPLICANT: Watson, Susan R.

APPLICANT: Britis Represser Sistemation of Cancer

TILLE OF INVENTION: Methods of Screening for Modulators of Cancer

TILLE OF INVENTION: Methods of Screening for Modulators of Cancer

TILLE OF INVENTION: Methods of Screening for Modulators of Cancer

TILLE OF INVENTION: Methods of Screening for Modulators of Cancer

TILLE OF INVENTION: Methods of Screening for Modulators of Cancer

TILLE OF INVENTION NUMBER: US 09/663,733

PRIOR APPLICATION NUMBER: US 60/335,394

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-15

PRIOR FILING DATE: 2001-11-15
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PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR PILING DATE: 2001/03-14
PRIOR FILING DATE: 2001/03-26
PRIOR FILING DATE: 2001/03/26
PRIOR FILING DATE: 2001/03/26
PRIOR FILING DATE: 2001-03-10
PRIOR FILING DATE: 2001-03-26
PRIOR FILING DATE: 2001-09-26
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PRIOR FILING DATE: 2001-09-13
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Publication No. US20030232350A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 243; Conservative
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US-10-097-340-135
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APPLICANT: Shubhangi KAWATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Steve G. KOVATS
APPLICANT: Michael HORRISEY
APPLICANT: Michael HORRISEY
APPLICANT: Michael HORRISEY
APPLICANT: Ami SEN
APPLICANT: Peter VILBY
APPLICANT: Racen LU
APPLICANT: Karen GLATT
APPLICANT: Karen GLATT
APPLICANT: Karen GLATT
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REPRESENCE: MRI-030
                                                                                              Sequence 1, Application US/10045992
; Sequence 1, Application US/10045992
; Publication No. US20020161211A1
; GENERAL INFORMATION:
; APPLICANT: LINDMEN; Volkhard
; APPLICANT: ELINDMEN; VOLKhard
; TITLE OF INVENTION: CONPOSITIONS, METHODS AND KITS RELATING TO REMODELIN
; FILE REFERENCE: 053689-5006-01
; CURRENT APPLICATION NUMBER: US/10/045,992
; CURRENT FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/9692,081
; PRIOR PILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 9-10-1
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 243
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CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 135, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAWATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
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Matches 243; Conservative
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ORGANISM: Homo sapiens
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241 LPK 243
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Sequence 1173, Application US/10295027

Publication No. US20030232350A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Ginsberg, Wendy M.

APPLICANT: Gish, Kurt C.

APPLICANT: Gish, Kurt C.

APPLICANT: Hevezl, Peter A.

APPLICANT: Hevezl, Peter A.

APPLICANT: Marck, David H.

APPLICANT: Marcy, Richard

APPLICANT: Watson, Susan R.

APPLICANT: Watson, Susan R.

APPLICANT: Bos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Biagnosis of Cancer,

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer,

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer,

CURRENT PILING DATE: 2000-09-15

PRIOR PILING DATE: 2000-09-15

PRIOR FILING DATE: 2001-11-13

PRIOR FILING DATE: 2001-11-13

PRIOR PILING DATE: 2001-11-13

PRIOR PILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-21
PRIOR PLILING DATE: 2001-11-29
PRIOR PLILING DATE: 2001-11-29
PRIOR PELICATION NUMBER: US 60/340,376
PRIOR PELICATION NUMBER: US 60/347,211
PRIOR PLILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-01-08
PRIOR PLILING DATE: 2002-02-08
PRIOR PLILING DATE: 2002-02-08
PRIOR PLILING DATE: 2002-02-08
PRIOR PLILING DATE: 2002-02-13
PRIOR PLING DATE: 2002-02-13
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100.0%; Score 1303; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-50
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US-10-295-027-1173
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is Sequence 74, Application US/10173999

j. Publication No. US20040005563A1

j. Sequence 74, Application US/10173999

j. Publication No. US20040005563A1

j. GENERAL INFORMATION:

j. APPLICANT: Mack, David H.

j. APPLICANT: Gish, Kurt C.

j. APPLICANT: Gish, Kurt C.

j. APPLICANT: Bos Biotechnology, Inc.

j. APPLICANT: Bos Biotechnology, Inc.

j. TITLE OF INVENTION: Methods of Sizeening for Modulators of Ovarian

j. TITLE OF INVENTION: Cancer

j. FRIOR REFERENCE: 08501-06-17

j. PRIOR APPLICATION NUMBER: US 60/299,234

j. PRIOR APPLICATION NUMBER: US 60/315,287

j. PRIOR APPLICATION NUMBER: US 60/315,287

j. PRIOR APPLICATION NUMBER: US 60/315,246

j. PRIOR FILING DATE: 2001-04-12

j. PRIOR FILING DATE: 2001-04-12

j. NUMBER OF SEQ ID NOS: 163

j. SUGTWARE: Patentin Ver. 2.1

j. SEQ ID NO 74
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PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PELING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-24
PRIOR PILING DATE: 2001-12-14
PRIOR PILING DATE: 2001-12-14
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-01-10
PRIOR PELING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
PRIOR FILING DATE: 2002-02-13
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Best Local Similarity 100.0
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1173
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CRGANISM: Homo sapiens
US-10-295-027-1173
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121 GKIAECTFTKWRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
                                                                                                          181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
                                                                                                                                                                                                          181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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Publication No. US20040076955A1
GENERAL INFORMATION:
APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha
APPLICANT: Ess Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/10634108
Publication No. US2004006317641
Publication No. US2004006317641
APPLICANT: LINDMEN, Volkhard
APPLICANT: ENIESEL, Robert F.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO REMODEL
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS CURRENT APPLICATION NUMBER: US/10/634,108
CURRENT APPLICATION NUMBER: US/09/692,081
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
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US-10-634-108-4
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sequence 38, Application US/20040029114A1

sequence 38, Application No. US20040029114A1

sequence 38, Application No. US20040029114A1

septicant: Mary Experiment Gish, Kurt C.

APPLICANT: Mary Daniel

APPLICANT: Afar, Daniel

APPLICANT: Afar, Daniel

TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer

TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer

TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer

TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer

TITLE OF INVENTION: Methods of Screening for Modulators of Breast Cancer

CURRENT APPLICATION NUMBER: US 60/263,965

PRIOR PILING DATE: 2001-01-24

PRIOR PILING DATE: 2001-04-09

PRIOR PILING DATE: 2001-04-09

PRIOR PILING DATE: 2001-04-09

PRIOR PILING DATE: 2001-04-09

PRIOR PILING DATE: 2001-05-04

PRIOR PILI
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                                                                                                                                                                                     0; Indels
                                                                                                                                  Query Match 100.0%; Score 1303; DB 4; Best Local Similarity 100.0%; Pred. No. 1.6e-115; Matches 243; Conservative 0; Mismatches 0;
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100.0%; Score 1303; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-115,
Matches 243; Conservative 0; Mismatches 0;
     ; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-173-999-74
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US-10-058-270A-38
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LPK 243
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US-10-058-270A-38
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APPLICANT: Karen LU

APPLICANT: Karen ZHAO

APPLICANT: Xumei ZHAO

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
FILE REPRENCE: MRI-030

CURRENT APPLICATION NUMBER: US/10/097,340

PRIOR APPLICATION NUMBER: US/10/097,340

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR PILING DATE: 2001-03-14

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-19

PRIOR PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-09-19
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                                                                                                                                                           61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
                                                                                                                                                                                              61 GVPGRDGSPGANGIPGTPG1PGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
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                                                                            1 MRPQGPAASPQRLRGLLILILLIQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA 60
                                              MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASBIPKGKQKAQLRQREVVDLYNGMCLQGPA
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SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 135, Application US/11050926
Publication No. US20050214831A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karen LU
Rosemarie SCHMANDT
Xumei ZHAO
Karen GLATT
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Robert C. BAST, Jr.
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Rachel B. MEYERS
Michael MORRISEY
Peter OLANDT
Ami SEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peter VEIBY
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241 LPK 243
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sequence 4, Application US/10939233
sequence 6, Application No. US20050147602A1
sexpectation No. US20050147602A1
sexpectation No. US20050147602A1
sexpectation No. US20050147602A1
sexpectation No. US2005014
sexpectation No. US20051710NS, METHODS AND KITS RELATING TO CTHRC1, A NOVEL
stille OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO CTHRC1, A NOVEL
stille OF INVENTION: MODULATOR OF COLLAGEN MATRIX
stille OF INVENTION: WOMBER: US/10/939,233
current Application NUMBER: US 09/692,081
sprior Application NUMBER: US 10/045,992
sprior Application NUMBER: US 10/045,992
sprior Application NUMBER: US 10/045,992
sprior Application Number: Discourse 17
ssorthwar: Patentin version 3.2
ssorthwar: Patentin version 3.2
sego ID NO 4
LENGTH: 243
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CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR PILING DATE: 2001-00-3
PRIOR FILING DATE: 2001-00-3
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-08-03
PRIOR PLING DATE: 2001-11-08
PRIOR PLING DATE: 2001-11-08
PRIOR PLING DATE: 2001-11-3
PRIOR PLING DATE: 2001-11-3
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PLING DATE: 2001-11-13
PRIOR PLING DATE: 2001-11-13
PRIOR PLING DATE: 2001-01-15
PRIOR PLING DATE: 2001-01-15
PRIOR PLING DATE: 2001-01-15
SEQ ID NO 175
LENGRIH: 243
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US-10-188-832-175
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CORGANISM: Homo sapiens
US-10-939-233-4
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Gaps

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APPLICANT: PUSZCEAL, Lajos
APPLICANT: PUSZCEAL, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Ayesqual
APPLICANT: Mills, GORGOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: COMPOSITIONS, KITS, AND THERAPY OF BREAST CANCER
FILLE REPERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                           61 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDL 120
                                                                                                                                                                                                              96 GVPGRDGSPGANGIPGTPGIPGRDGFKGEKGECLRESFEESWIPNYKQCSWSSLNYGIDL 155
                                                                                                                                                                                                                                                                             121 GKIAECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 180
                                                                                                                                                                                                                                                                                                                            156 GKIABCTFTKOMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIIYLDQ 215
                                                                                                                                                                                                                                                                                                                                                                                                         216 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVALWVGTCSDYPKGDASTGWNSVSRIIIEE 275
                                                                                                       36 MRPQGPAASPQRLRGLLLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
                                                                                                                                                                                                                                                                                                                                                                                 181 GSPEMNSTINIHRISSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE
                                                                       1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
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                     Indels
Pred. No. 1.9e-115;
Best Local Similarity 100.0%; Pred. No. 1.9
Matches 243; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001-06-21
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-06-27
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PRESEQ FOR WINDOWS Version 4.0
SSOFTWARE: PRESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 496, Application US/10177293; Publication No. US20030124128A1; GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Clatt, Karen
APPLICANT: Zhao, Xumei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xu, Yongyao
Hoersch, Sebastian
Monahan, John
Meyers, Rachel E.
Bast Jr., Robert C.
Hortobagyi, Gabriel N
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Kamatkar, Shubhangi
Mertens, Maureen
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CORGANISM: Homo sapiens
US-10-177-293-496
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TITLE OF INVENTION: Nucleic Acid Molecules and Therapy of Ovarian Cancer
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REPRESENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT PILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-10
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR PRILING DATE: 2001-09-26
PRIOR PLING DATE: 2001-09-26
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181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVALWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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                                                                                                    1 MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
                                                                       1 MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
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                          0; Indels
100.0%; Pred. No. 1.6e-115; tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 131
LENGTH: 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebsetian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISER
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Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
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Best Local Similarity 100. Matches 243; Conservative
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ORGANISM: Homo sapiens
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Karen GLATT
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TYPE: PRT

ORGANISM: Homo sapiens
US-10-296-115-1261
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: ALBEGEL, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITION, ASSESSMENT, PREVENTION, AND TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2NM
FILE REFERENCE: MPMO1-029P2NM
CURRENT APPLICATION NUMBER: US 60/330,971
PRIOR APPLICATION NUMBER: US 60/330,971
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 77
LENGTH: 278
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                                                                                                                                                     96 GVPGRDGSPGANGIPGTPGIPGRDGPKGEKGECLRESPEESWTPNYKQCSWSSLNYGIDL 155
                                                                                                                                                                                                                                                                                     181 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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                                                                              36 MRPQGPAASPQRLRGLILLLLLQLPAPSSASEIPKGKQURQRRQURQREVVDLYNGMCLQGPA 95
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al Similarity 100.0%; Pred. No. 1.9e-115; 243; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 77, Application US/10301822; Publication No. US20030148410A1; GENERAL INFORMATION: APPLICANT: Millennium Pharmaceuticals, Inc.; APPLICANT: Berger, Allison
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CRGANISM: Homo Sapiens
US-10-301-822-77
Best Local Similarity
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US-10-301-822-77
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RESULT 15
US-10-296-115-1261

i Sequence 1261, Application US/10296115

i Sequence 1261, Application US/10296115

i Publication No. US20040053248A1

i GENERAL INFORMATION:

APPLICANT: Hyseq Inc

TILLE OF INVENTION: No. US20040053248A1e1 Nucleic Acids and Polypeptides

TILLE REFERENCE: 784PCT

CURRENT PAPLICATION NUMBER: US/10/296,115

CURRENT PAPLICATION NUMBER: US/9/488,725

PRIOR APPLICATION NUMBER: US/9/488,725

PRIOR FILING DATE: 2000-01-21

PRIOR PILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-04-25

NUMBER OF SEQ ID NOS: 1478

SEQ ID NO 1261
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                           216 GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVALWYGTCSDYPKGDASTGWNSVSRIIIEE 275
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GSPEMNSTINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEE 240
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